

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 99026

TO: Ashwin Mehta

Location: CM1/9E07/9E12

Art Unit: 1638

Monday, July 28, 2003

Case Serial Number: 09/991458

From: Toby Port

Location: Biotech-Chem Library

CM1-6A04

Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Mehta,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port



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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Oluntary Results Feedback Form
> I am an examiner in Workgroup: Example: 1610
> Relevant prior art found, search results used as follows:
102 rejection
103 rejection
☐ Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
☐ Foreign Patent(s)
Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention.
Comments:

Drop off or send completed forms to Stric/Biotech-Chem Library GMI — Circ. Desk



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STIC-Biotech/ChemLib

Fr	m:
Se	nt:

Mehta, Ashwin

Wednesday, July 16, 2003 5:50 PM STIC-Biotech/ChemLib

Subject:

seq search

STIC,

Please search the commercial and interference databases for the following from 09/991,458:

- 1) the nucleotide sequence of SEQ ID NO:1 2) the amino acid sequence of SEQ ID NO: 2

My mail room is 9E12, office 9E07, art unit 1638.

Thank you, Ashwin

Ashwin Mehta United States Patent and Trademark Office Biotechnology Patent Examiner 703-306-4540

Searcher:
Phone:
Location:
Date Picked Up:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

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SUMMARIES

Result 2860 2423.4 446.6 Score Match Query Length 167902 302786 70610 153352 202495 260967 184621 233148 37319 DВ AF286026 BTU09198 D AF109072 AE003645 DROSADH05 AF318177 BTNORADR AK096607 AF109391 MMU238309 RATDTRSP S80071) RATDOPER) RATLPTHA AF411042 AR048966 AC017561 AC093103 AC092246 AC018164 AC007440 AE003822 AC014400 AC104604 AE003434 AC010022 AC091203 AE003552 AY121662 AX191701 Ħ AR080685 AX191697 AC018319 AX191697 Sequence AX121662 Drosophil AX191701 Sequence AX071318 Drosophil AX191701 Sequence AX071318 Drosophil AX191703 Sequence AF369383 Aedes aeg AC015177 Drosophil AC007330 Drosophil AC007894 Drosophil AR048966 Sequence AR080685 Sequence L21672 Rat mRNA se AF286026 Macaca mu U09198 Bos taurus AF199072 Mus muscu X79015 B. taurus mR AK096607 Homo sapi AF109391 Mus muscu AJ233309 Mus muscu M80233 Rat cocaine S80071 hpROT-brain M80570 Rat dopamin M88111 Rattus norv AC092246 Drosophil AE003645 Drosophil AE003411 Drosophil AF318177 Danio rer AF411042 Mus muscu Description AF013963 Manduca s AF006063 Manduca s AY060329 Drosophil Drosophil

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ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	RESULT 1 AF013963
1 (bases 1 to 2860) Feldman,D.H., Harvey,W.R. and Stevens,B.R.	Bukaryota; Metazoa; Artnropoda; Hexapoda; Lisecta; Freilyera; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea; Sphingidae; Sphinginae; Manduca.	Manduca sexta	Manduca sexta.		AF013963.2 GI:16356923	AF013963	sodium/potassium ions (CAATCH1) mRNA, complete cds.	Manduca sexta amino acid transporter/amino acid gared channer for	AF013963 2860 bp mRNA linear inv 30-001-2001	

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	21 CGGCGGTTTCGAGTCGTCGGAGCCCAAGATGGAACCAAAACGATCATCGCAAATAAGTTT 180 	61 ATACACCTAAACACATTGCAAGTGTGATATTGTGGACAAAATGAATG	1 GGCACGAGGTTACTTGTTGGAGGAACTGTTTGGCGGTGGTGCGATCGAT	Match 100.0%; Score 2860; DB 3; Length 2860; Local Similarity 100.0%; Pred. No. 0; Length 2860; Gaps 0; es 2860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TGAYRRIN' 780 a 608 c 598 g 874 t	FSVLFFILMSVLGIGSSVALLGFERUTLAMDAFREVPTVMSAMTCSGFELIGLTYCTP GGQYILELVDHYGGTFLVLFCAISELAGVFWIYGLENLCLDIEMLIGKTGAVWALCW GVITPAIMTTVFFYALLASNNLVEGDNYVYPTAGYVGYLMLFLGMTFVPIGIGFSLY KVPTGTAGETIIVA EMTENGYANGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	SFOATLERAALOQEWENCY SONS YNWS 18 FAMKGIG FALARGIGGY ILSYYVY ICGLCLYYLAM SFOATLERAALOQEWENCYPSDETLAASYNIN INGTSSAOLYFELTULQQSDG IEGGL GAPIWYLVLCLE IAWLMVFGVVARGVKSSGKAAYFLALEPYVVMITLETITIILJGAT DGILFFVTDOMAKLLELGWWYSAYTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIV	/db_xref="GI:6594619" /db_xref="GI:6594619" /translation="MNDGQVNGGFESSEPKMEPKRSSQISLPPANNKAALDNIDDTDL EAEPPERNYWSNNIEFLMSCIATSVGCHVWRFPPIAYQNGGGAPLVPYVIVLLLVGK PVVVLCTVLGOFCSENTUSVJSTSTORVCGTVFTAYQNGGGAPLVPYVIVLLLVGK	/codon_start=1 /codon_start=1 /product="amino acid transporter/amino acid-gated channel for sodium/potassium ions" /protein id="aari918560 1"	orter with multiple funct	/dev_stage="5th instar larva midgut" /note="common: tomato hornworm" 1. 2860 /gene="calrun"		S.W. Archer Rd., Gainesville, Ft. 32607, USA Sequence update by submitter On Oct 24, 2001 this sequence version replaced gi:6594618.		sion -AUG-1998) d., Gainesy	Submitted (14-JUL-1997) Physiology, University of Florida, 1600 S.W. Archer Rd., Gainesville, FL 32607, USA 3 (bases 1 to 2860) W. And Stavens B B Feldman, D. F., Harvey W. and Stavens B B	10829035 2 (bases 1 to 2860) Feldman,D.F., Harvey,W. and Stevens,B.R.	A novel electrogenic amino acid transporter is activated by K+ or Na+, is alkaline pH-dependent, and is Clindependent J. Biol. Chem. 275 (32), 24518-24526 (2000)
Qy	Qу	Qy Db	Дb	Дy	Дb	Db Qy	ОУ V9	Db	D Vy	Db	Дb	Оb	Ду	Db Qy	Db	D Qy	D 45	Db
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Sphingiodea; Sphingidae; Sphinginae; Manduca.

1 (bases 1 to 2881)
Castagna, M., Shayakul, C., Trotti, D., Sacchi, V.F., Harvey, W.R.
Hediger, M.A.
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Submitted (30-MAY-1997) Renal Division, Department of Medicine,
Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115,
USA
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="Fiybase:fbgn0033443"
/translation="METTINNNNNDNOTMNOAYVGSLNASTISIPGAYKPNESSNGKK
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TLSEGGSAPPPGHGDSPSGVEAGQOCKKRDSWNDLEFLMSCIALSYGLGNVWRFPF
TALENGGGAFVIPYLIVLILVGKPYYLEMLLGQFSSRGSVKVYDESPIMRGIGYGQV
TATGIYTTYYAATLMALTLRYFVDSFYPFLFWSYCREEMGTECLDSGPQDASRATSLAG
TATGIYTTYYAATLMALTLRYFVDSFYPFLFWSYCREEMGTECLDSGPQDASRATSLAG
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ASYFLALFPYVVMLVLLVRALTLPGAFDGVLYFLRPQWHKLLEFQVWYAAVTQVFFSL
AICEGNIIMYASYNRFGHNIYRDANIYTTLDTETSLLSGVIJEGLGNLAYENTTDI
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SGVYVFGWCLSAFGVGQVLFWAIPAVRKQPSHLGLWARIRKAFEPLPNWGPSDPQTLK
                                                                                                                                                                                                                                                                                                                                     ASVVNGGPGLAFISYPDAIAKFKWLPQLFSVLFFLMLFVLGIGSNVGMASCMSTVIKD
QFGHLKNWTVVVGIAIVGYFLGLLYITPGGQFLLNLVDYFGVTFVALVLAIFELVTIA
                                                                                                                                                                                            RYQLEVQEGNANALFRRSSIWHKIYDNIFG"
1010 c 1005 g 1048 t
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/db_xref="FLYBASE:FBgn0033443"
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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Score 446.6; Ub ...
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Matches Query Match Best Local

850;

Conservative

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Similarity

15.6%;

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TCCGTGGCTATCGACTTTCAACACATTGGCGATGGACGCGTTCCCACGTGTACCC
                                                    AATGGAGGTCCGGGCCTTGGCTTTCATATCTTACCCGGACGCCATTGCCAAGTTTAAGTGG
                                                                                                                                           GCTGSCGGTACCAGTCTTGCATTTCATACCCTGATGCCATTGCCAA----AACATTC
                                                                                                                                                                                                                                                                                          GATGCTTGGATTGTTACGACTTTGGACACCTTTACAAGTTTCTTGTCTGGGTGCACGATC
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Sequence 3
AX191697
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Patent: WO 0149848-A 3 12-JUL-2001;
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Nucleic acids and polypeptides of drosophila melanogaster snf sodi
sodium-neurotransmitter symporter family cell surface receptors an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Ptery
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorph
Ephydroidea; Drosophilidae; Drosophila

(bases 1 to 2473)
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                             GTCGGCAAGCCTGTGTACTACTTAGAGTGTGTCTCTCGGACAATTCAGTTCAAGAAACTCT
                                                                                                ATCGCGTACCAGAATGGAGGAGGTGCTTTCCTGGTGCCATACGTCATCGTTCTTTTACTT 397
                                                                                                                                                    TTTCTAATGTCCTGCATATCGGTGTCCCTTGGGCATCGGCAACGTTCCCGTTC
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           ATCGGCAAACCCATGTACTATTTGGAGATGATCATGGGCCAGTTCACGAGCCAGGGAACG
                                                                              ACGGCCTATGAGAATGGAGGAGGCGCCTTCCTTATACCCCTACATCATAGTGCTCTTTCTG
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/db_xref="taxon:7227"
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KEYWORDS SOURCE DEFINITION ACCESSION RESULT 5 AY121662 LOCUS VERSION ORGANISM Drosophila melanogaster AY121662 AY121662.1

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18-JUN-2002

REFERENCE AUTHORS Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 2497) Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Insecta; Pterygota; era; Muscomorpha;

Carlson, J

TITLE JOURNAL

Submitted (13-JUN-2002) Berkeley Drosophila Lawrence Berkeley National Laboratory, One C Berkeley, CA 94720, USA Sequence submitted by:

Berkeley Drosophila Genome Project Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patell, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. Direct Submission and Celniker,S Cyclotron Genome Project, Cyclotron Road,

COMMENT

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Lawrence Berkeley National Laboratory Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular CDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns priming, priming from contaminating genomic DNA, retained introduce to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to

Qy 518 Db 658 Qy 578 Db 718 Db 778 Db 778 Qy 643 Db 838 Qy 695	Db 418 Qy 338 Db 478 Qy 398 Db 538 Qy 458 Db 598	Query Match Best Local s Matches 951 Qy 218 Db 358 Qy 278	BASE COUNT	CDS	FEATURES SOURCE gene
8 TGCGGTTACATCCTGTCTTACGTACGTGGTGATCTGTGTGTCTGTATTACTTAC	•	Ch 13.7%; Score 391.8; DB 3; Length 2497; 1 Similarity 53.2%; Pred. No. 8.6e-75; 951; Conservative 0; Mismatches 767; Indels 69; Gaps 3; 9518 GATGACACGGACTTAGAGGCTGAACCGCCAGAACGTATGGTATGGTCCAACAACATTGAA 277	/notes" Longest ORF" /codon_start= /codon_start= /product="REL0560p" /product="REL0560p" /product="REL0560p" /protein_id="RAM51989.1" /db_xref="REL0560p" /db_xref="REL0560p" /db_xref="REL05406472" /db_xref="FLYBASE:FBgn0029762" /translation="MELKGVQPSNGSSNGSGNGATNAASTEKTDAEKPTAERTNWGNG /translation="MELKGVQPSNGSSNGSGNGATNAASTEKTDAEKPTAERTNWGNG /translation="MELKGVQPSNGSSNGSGNGATNAASTEKTDAEKPTAERTNWGNG /translation="MELKGVQPSNGSSNGSGNAYFILALFYXYLEVSFQSELPWSYCRD EMTNCYUSRFQPSVDNLLTGVSLANESARNLSGIVANDETEKLOSSSELPFLNVVLIE KLDISOGVGDDWKLTLALFVAMVVIFLVIMRGVKSSGKAAYFILALFPYVVLIFVLLIR AVTLEGARDGILFFLEPGMGELLNPTVWKEAVVQEFSSLAVGSSGPIIMFASYNNEPDHG IYRDAMIVTTLDTLTSSLLGGTTIFAILGULAHNIQIENIRDVURSGTGLAFISYDDAI SKFQAVPQLFSVLFFFMLFVLGIGSIVALQSTIVTIICDQFKGKYMKYALTTSVCGF LMGLVYVTPGGGGMILTLVDFYGGTYVVFILATFELAGIVWVYCLQNFCDDIEEMCNRR VSLYMRVGMSFFTPVMMIIFIYSMVTIEDIKYSELYFPEANNIAGMLLFAIGAAQFP LMGLWYSRFTPGTYMKSLKASSLKPSDRWGPANPEIRREWVIFKNQKAAQRATQKGTS KLGFFMRKVANFCGSNK" 625 a 604 c 636 g 632 t	/db_xref="FLYBASE:FBgn0029762" 2802205 /gene="CG3252"	cdna@fruitfly.berkeley.edu. Location/Qualifiers 12497 /organism="Drosophila melanogaster" /strain="y; cn bw sp" /db_xref="taxon:7227" 12497 /gene="C3353"
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 ATTGAGTTCATGTTGGGTAAAAAGACTGGTGCTTACTGGCGTCTCTGCTGGGGGGCGTAATC
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RESULT 7
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KEYWORDS FLI
SOURCE Droc

AY071318

ON Drosophila melanogaster RE34084 full length cDNA.

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FLI_CDNA.

Drosophila melanogaster.

Query M Best Lo Matches Qy Db	BASE COUNT.	Ω 4 9	SOU SOU		TITLE JOURNAL COMMENT	ORGANISI REFERENCE AUTHORS
Query Match 13.4%; Score 382.8; DB 3; Length 2099; Best Local Similarity 54.0%; Pred. No. 7.8e-73; Best Local Similarity 54.0%; Pred. No. 7.8e-73; Matches 872; Conservative 0; Mismatches 732; Indels 10; Gaps 4; 260 TGGTCCAACAACATTGAATTCTTGATGTCCTGCATCGCTACATCCGTCGGTTTGGGTAAC 319	/Godon_start=1 /Godon_start=1 /Codon_start=1 /product="Re34040.1" /protein_id="AAL48940.1" /protein_id="AAL48940.1" /protein_id="AAL48940.1" /db_xref="FLYBASE:FB9N0033708" /db_xref="FLYBASE:FB9N0033708" /db_xref="FLYBASE:FB9N0033708" /Lranslation="MGGAGGSREGHPGSNDGISTVIYSAEGEELTINCEAESESSGQR /Lranslation="MGGAGGSREGHPGSNDGISTVIYACIMALTIRYLVASFSEVLP UIGQFSSRGCIRAFDMAPIMRGIAYGQVYSTALATTYYACIMALTIRYLVASFSEVLP WTYCLVEWGKSCVATGATAANDSSIVGGVSSAELFFTQTVLREPESIDDNGLGTPSWD LVLCLLARWVIIGTILSKGIRSSGKASYFLALFFYVMITYLLIRAVTLPGAMQGIYF LKPQWSOLLNPHVWYAAITQMFFSLAICFGTLVMYASFNDFNKNVHKDVIIITTIDSL TSILAGCIIFGIIGANLAFFTNTKDISQVVKGGAGLAFISYPEAIAKFKYLPQLFAVLF FFMLLVLGIGSNIGMASAGGECG" FFMLLVLGIGSNIGMASAGGECGF 598 t	gene 12099 //gene="CG8850" /note="alignment with genomic scaffold AE003822" //db_xref="FLYBASE:FBgn0033708" CDS 941341 //cos="Note: Section of the cost of t	rce	Herkeley, CA 94720 This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal due to reverse transcriptace contaminating genomic DNA, retained introns reverse transcriptace errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to	AL .	ORGANISM Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Ephydroidea; Drosophila. I (bases 1 to 2099) AUTHORS Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
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Sequence submitted by:
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1 (bases 1 to 2097)
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                                                                   cdna@fruitfly.berkeley.edu.
                                                                                           and relationship to other sequences,
(http://fruitfly.berkeley.edu) or se
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                                                                                                                            please visit our Web site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACATTGAATTCTTGATGTCCTGCATCGCTACATCCGTCGGTTTTGGGTAACGTGTGGCG
                                                                                                                                                                                                                                                                                              AGCTGCCGGCTGCGGTTACATCCTGTCTTACTACGTGGTGATCTGTGGTCTCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCCCCTTTACTGCCCTCGATAATGGCGGTGGCGCCTTCCTCATACCATATCTCATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCCCTTTCATCGCGTACCAGAATGGAGGAGGTGCTTTCCTGGTGCCATACGTCATCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGATAATATAGATGACACGGACTTAGAGGCTGAACCGCCAGAACGTATGGTATGGTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACGGACGCAGTACGGCCAGCACAGTGGAGATTTCGACC----AACAGTCCAGCCCTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATTGTGGACAAAATGAATGACGGCCAAGTAAACGGCGGTTTCGAGTCGTCGGAGCCCAA 147
                                 GA---ACTGCGTACCCTCAGATC--
                                                                                                                                                                                                                                                                                                                                                                                                AAGAAACTCTGTTAAAGTTTGGTCAATTTCACCGGCCATGAAAGGTACTGGATACGCTCA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTTTACTTGTCGGCAAGCCTGTGTACTACTTAGAGTGTGTCCTCGGACAATTCAGTTC
                                                                                                 ATATTTCATTGAATCATTTCGCAACCCATTGCCCTGGTCCACATGCCGTGCGGAATGGGG
                                                                                                                                                                 TTACTTAGCTATGAGCTTCCAGGCCACTCTTCCATGGGCTATTTGTCAGCCTGAGTGGGA 627
                                                                                                                                                                                                                                                                                                                                                              TCGGGGCTCGGTTAAAGTGTTCGATTTGTGCCCGGCGATGAAAGGTGTTGGAGCTGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGTTCCTGATTGGCAAACCGATTTACTATCTGGAAATGGTAATTGGCCAGTTTTCCAG
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/db_xref="Fg1:16130
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LIAVVSFFIGLMYITPGGQYMLTLVDFFGASMIALVLGIAELYTIGWIYGTDRLCKDI
EFMLGRKVGLYWRLCMSIITPLIMTVILIYFYATYQPLTYNNIVYPNWSYSIGWLITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGILQLPIWMIVAIVRDPGQTLGAKIRGAFTPKKNWGPSDPLLREQYHKEIENELTPK
RGQGIWAAIKQNIFG"
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/note="alignment with genomic:
/db_xref="FLYBASE:FBgn0028886"
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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1657 GTTCTTCTACGCTCTTCTCGCCTCTAACAACCTGGTGTTCGGAGACAACTACGTATACCC
      1643 TCTGATCTA---TTTCTATGCGACCTACCAACCTCTAACATACAACAATATCGTCTATCC
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                                                                                                                                                                                                                                                                                                                                                 CATTCGGGATCGGTTTCCCCAACTTTGGGCAGTGGCAGTGCTCGCTGCTCATCGCTGTAGT 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACTCAGAGGTGGGAGATGTGGTGGGTGCTGGCGGTACCAGTCTTGCTTTCATTTTCATA 1239
                                                                                     AGTGGGCCTGTACTGGAGGCTCTGCTGGAGCATCATTACCCCGCTGATCATGACTGTTAT
                                                                                                                GACTGGTGCTTACTGGCGTCTCTCCTGGGGCGTAATCACTCCTGCTATAATGACGACTGT
                                                                                                                                                                           GTTCTGGATTTATGGATTGGAGAATCTGTGCCTAGACATTGAGTTCATGTTGGGTAAAAA 1596
                                                                                                                                                                                                                                                              GGACTTTTTCGGCGCCTCAATGATTGCTTTGGTACTGGGAATCGCCGAGCTGTACACCAT
                                                                                                                                                                                                                                                                                                AGATCACTACGGTGGAACATTCCTTGTGCGTTTTTCTGCGCCATTTCTGAACTCGCAGGGT
                                                                                                                                                                                                                                                                                                                                                                          CGGTTTCCTGCATGTTGTACTGCACACCGGGTGGACAATATATTCTTGAGCTTGT 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGATGGACGCGTTCCCACGTGTACCCACCGTCTACATGTCAGCGATGACCTGTTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATGCTCTTCGTGTTGGGCATAGGATCGAATATAGCCATGACCTCCTGCTCGGTGACCGC 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGATGTCGGTGCTGGGTATCGGCTCATCCGTGCTCTGCTATCGACTTTCAACACATT 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACAAGTTCGGGCACAATGTACACAGGGATGCAGCAATTGTAACGGGTCTGGACACTAT 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACGCAAGTGTTCTTCTCTGACAGTGTGCACCGGACCGATCATCATGTTCTCCTCTTA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACTTATAAAGCCGCAATGGGGAAAGATTTTGGACCCGAAGGTTTGGTACGCGGCTGT 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCATGGGTGTTCTTGGTGCGAGCTGTAACTCTGCCGGGATCAATAGACGGTATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGAACCGATGACATCGGCTCAGTTGTGAAGGGCGGTGCCGGATTGGCCTTCATCTCATA 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACAAGTTTCTTGTCTGGGTGCACGATCTTCGGTATCCTTGGTAACCTCGCGTACGAACT 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTCATGATCACTTTATTCATCACCACAATCATCCTGCCCGGTGCTACTGACGGCATCCT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGTCGCGGAGTGAAGAGTTCGGGAAAGGCATCCTACTTCCTGGCCCTTTTCCCGTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCCCGAGGAGTCAAGAGTTCCGGCAAAGCGGCCTACTTCCTCGCGCTCTTCCCCATACGT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCATCTGGTACTTGGTGTTGTGTCTATTCATCGCATGGCTCATGGTGTTTCGGAGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGCGCCCGCAAAATTACACAATGAAATCACAAAAACGATCGGGTCATCACCAGTTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACTCAGTGTTTCTACTCCTTGTCCGTTTGTTTCGGCAACATCATCATGTACTCCTCGTT 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCTTCGTCACGCCTCAATGGGCGAAACTCCTTGAGCTCGGTGTATGGTACTCAGCAGT 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTCTACTTTTTGAGAACAGTTCTCCAACAAGCGATGGAATTGAAGGAGGTCTCGGTGC
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Qy	Db	ОУ	db Yo	Qy Db	Db	D Qy	Db Qy	Db	Query Match Best Local Matches 97	FEATURES SOURCE BASE COUNT ORIGIN	JOURNAL	ORGANISM REFERENCE AUTHORS TITLE	RESULT 9 AX191703 LOCUS DEFINITION ACCESSION VERSION KEYMORDS SOURCE	Qу	Qy Db	dd £
508 AGCTGCCGGCTGCGGTTACATCCTGTCTTACTACGTGGTGATCTGTGGTCTCTGTCTG	394 TCGGGGCTCGGTTAAAGTGTTCGATTTGTGCCCGGCGATGAAAGGTGTTGGAGCTGGCCA 453	448 AAGAAACTCTGTTAAAGTTTGGTCAATTTCACCGGCCATGAAAGGTACTGGATACGCTCA 507	388 TCTTTTACTTGTCGGCAAGCCTGTGTACTACTTAGAGTGTGTCCTCGGACAATTCAGTTC 447	328 GTTCCCTTTCATCGCGTACCAGAATGGAGGAGGTGCTTTCCTGGTGCCATACGTCATCGT 387	268 CAACATTGAATTCTTGATGTCCTGCATCGCTACATCCGTCGGTTTGGGTAACGTGTGGGG 327 	208 GGATAATATAGATGACACGGACTTAGAGGCTGAACCGCCAGAACGTATGGTATGGTCCAA 267	148 GATGGAACCAAAACGATCATCGCAAATAAGTTTACCTCCAGCAAATAATAAAGCGGCTCT 207	88 TATTGTGGACAAAATGAATGACGGCCAAGTAAACGGCGGTTTCGAGTCGTCGGAGCCCAA 147 	watch 13.2%; Score 378.6; DB 6; Length 2108; Local Similarity 53.2%; Pred. No. 6.4e-72; Local Sometive 0; Mismatches 799; Indels 58; Gaps 6;	Locat. 12 ye 12 /organ /db_x: 524 a 55	methods of use Patent: WO 0149848-A 9 12-JUL-2001; Genontera LIC (MS)	u Drosophila Eukaryota; Neoptera; Ephydroide; 1 (bases: Kellerman; Nucleic ac: sodium-neu		1837 AGCCTTCCAAACCCTCATGGGGTCCCCG 1869	1777 TGGAATTGGATTITCTTTGTACAAATACCGTACCGGAACCTTCAGCGAGACGATCAAGAA 1836	

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Reoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
1 (bases 1 to 1996)
Dasher, M.K., Kohn, A.B., Harvey, W.R. and Stevens, B.R.
Dashar, A Novel Amino Acid Transporter from Larval Aedes aegypti
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/protein_id="ami3400.1"
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NSTSGOKVSSOIYFLDIVLKEKDSIDDGIGAPDWLTILMGHTFILLGGWTIFSILGNLAHHUGI
FSLSVGMGSIIMFSSYNNFHHNIYRDAMIVTTLDTFTSLLGGWTIFSILGNLAHHUGI
FSLSVGMGSIIMFSSYNNFHHNIYRDAMIVTTLDTFTSLLGGWTIFSILGNLAHHUGI
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FWDAFFKKYWHLALLISTIGFCTGLVYIHVANGYSTWSITTEAFSDLRLAIIEWVA
IFWIYGLDNWCNDIEFWVQRRVGLYVAAMLGSNNATFHDCRFHLFLVEYKWPTYSGOQ
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/db_xref="taxon:7159"
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Location/Qualifiers
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                                                                                                           CTTCCACTCCAAACCCTCATGGGGTCCCCGCTCGCCGAGAGAGCGTAGAGAATGGATGCA
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BASE COUNT ORIGIN This sequence was identified as CDM:10211923 by For further information on this sequence e-mail * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is avai

* the accession number will be preserved. Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 66809) Adams, M. and Vente Direct Submission Drosophila melanogaster, *** Rockville, MD, USA Submitted (16-NOV-1999) Celera Genomics, HTG; HTGS_PHASE2 AC015177.1 GI:6436158 AC015177 19034 and Venter, J.C. /organism="Drosophila melanogaster" /db_xref="taxon:7227" Location/Qualifiers O 14832 g 18339 bp DNA SEQUENCING Ä 45 Insecta; Pterygota; linear PROGRESS available West Gude Muscomorpha; the submitter. to fly@celera. fly@celera.com ***, in ordered Drive,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCACTGGCTGTGGCCTGGATCGTCATCGCGGGGATTATGTTCAAGGGTGTGAAGAGTT
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GCGGTCGTCACTCCTGCTAATGCTCACCATTCTCACCACCTTGGTTCTGTACGAG
                             GGCGTAATCACTCCTGCTATAATGACGACTGTGTTCTTCTACGCTCTTCTCGCCTCTAAC 1684
                                                                                               TGCCTAGACATTGAGTTCATGTTGGGTAAAAAGACTGGTGCTTACTGGCGTCTCTGCTGG 1624
                                                                                                                                CTGGTGCTGGCCATCTTCGAGCTGGTGACCATTGCCTGGATCTACGGTGTGAAGCGACTC
                                                                                                                                                             CTTTTCTGCGCCATTTCTGAACTCGCAGGCGTGTTCTGGATTTATGGATTGGAGAATCTG
                                                                                                                                                                                                ACACCCGGTGGCCAGTTCCTGCTCAACCTGGTCGACTACTTTGGCGTCACGTTCGTGGCC
                                                                                                                                                                                                                               ACACCGGGTGGACAATATATTCTTGAGCTTGTAGATCACTACGGTGGAACATTCCTTGTG
                                                                                                                                                                                                                                                                  AACTGGACTGTGGTTGGTATAGCCATTGTAGGCTACTTTCTGGGCCTTCTGTACATC
                                                                                                                                                                                                                                                                                                 ACCGTCTACATGTCAGCGATGACCTGTTCTTGCGGTTTCCTGCTTGGACTTGTTTACTGC
                                                                                                                                                                                                                                                                                                                                                                 TCCGTGGCTCTGCTATCGACTTTCAACACATTGGCGATGGACGCGTTCCCACGTGTACCC
                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCGCAGCTATTCTCCGTGCTGCTTCTTCCTCATGCTCTTCGTCCTGGGCATCGGCAGC
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56.2%;
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Pred. No. 3.2e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kin, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeliffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Woshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Seguencing of Drosophila chromosome 2R, region 46C-46D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC007330 ID0054 WF Drosophila melanogaster, chromosome BACR30G11, complete sequence.
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1 (bases 1 to 166854)

Celniker, S. E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Mar 10, 2001 this sequence version replaced gi:6957975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-APR-1999) Drosophila Genome Center, Laboratory, MS 64-121, Berkeley, CA 94720, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           archive Web site (http://www.fruitfly.org/sequence/) or
to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was assembled using end sequences from a whole genome
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                                                                                                                                                                          Drosophila melanogaster BAC
                                                                                                                                                                                                       /clone="BACR30G11 (D600)"
/clone_lib="RPCI-98 (Roswe
                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/strain="y; cn bw sp"
/db_xref="raxon:7227"
/chromosome="2R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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   274.6;
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Muscomorpha;
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, Busam,D.A.,
Dietz,S.M.,
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      AACCTGGTGTTCGGAGACAACTACGTATACCCGACTGCT 1723
                                                                                                                                                                GGCGTAATCACTCCTGCTATAATGACGACTGTGTTCTTCTACGCTCTTCTCGCCTCTAAC
                                                                                                            GCGGTCGTCACTCCTCTGCTAATGCTCACCATTCTCATCTACACCTTGGTTCTGTACGAG
                                                                                                                                                                                                                                             TGCCGTGACGTGGAGTTCATGATTGGCATCAAGACTTCGCTGTACTATCGCATCTGCTGG
                                                                                                                                                                                                                                                                                   TGCCTAGACATTGAGTTCATGTTGGGTAAAAAAGACTGGTGCTTACTGGCGTCTCTGCTGG 1624
                                                                                                                                                                                                                                                                                                                                                                                                                           CTTTTCTGCGCCATTTCTGAACTCGCAGGCGTGTTCTGGATTTTATGGATTGGAGAATCTG 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACTGGACTGTGGTGGTATAGCCATTGTAGGCTACTTTCTGGGCCTTCTGTACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACCTCAGCTATTCTCGGTGCTGTTCCTTCCTGATGATGTCGGTGCTGGGTATCGGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                 CTGGTGCTGGCCATCTTCGAGCTGGTGACCATTGCCTGGATCTACGGTGTGAAGCGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACCCGGTGGCCAGTTCCTGCTCAACCTGGTCGACTACTTTGGCGTCACGTTCGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCGTCTACATGTCAGCGATGACCTGTTCTTGCGGTTTCCTGCTTGGACTTGTTTACTGC 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGTGGGCATGGCCTCCTGCATGTCCACCGTGATCAAGGATCAGTTCGGACACCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCCGCAGCTATTCTCCGTGCTGTTCTTCCTCATGCTCTTCGTCCTGGGCATCGGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCGGTATCCTTGGTAACCTCGCGTACGAACTCAGAGGTGGGAGATGTGGTCGGT 1207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTGCGCGAGAAGGCGAGCATCGATGATGGCATCGGATATCCCAGCTGGAGCCTGGCGC
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0; Mismatches 409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chewe, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Punch, E., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clasiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Paciba, J.M., Park, S., Pfeiffer, B., Poon, L., Punch, E., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R., Stirskas, R., St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu
P1 library locations: 1-50, 2-95, 56-89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC005894 196337 bp DNA Drosophila melanogaster, chromosome 2R, DS00050, DS00191, and DS05369, complete AC005894 AC005435 AC005431 AC005441 AC005894.1 GI:3818342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (31-OCT-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Rc Berkeley, CA 94720, US Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 196337)
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                                  Similarity
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      Conservative
                                                                                                                                                                           þ
                                                                                                                                                                                                   /clone_lib="Pl library, partial Sau3A in pAd10sacBII" /note="These Pls, DS00050 (D349) DS00191 (D345) DS0536 (D355) were completed as a project DS00050 extends frr Pl end at bp 1 to Pl end at bp 79763. DS00191 extends from Pl end at bp 68,333 to Pl end at bp 154,851 DS05 extends from Pl end at bp 109,192 to Pl end at bp 196,337."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/strain="y2; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .196337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="P1s DS00050 (D349), DS00191 (D345),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="46A1-46B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                               9.6%;
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                                                                                                                                                                42152 g
0;
                               Score 274.6; DB 3
Pred. No. 3.2e-49;
   Mismatches
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                                                              Length 196337;
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Gaps
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                                                                                                                                                                                      GGCGTAATCACTCCTGCTATAATGACGACTGTGTTCTTCTACGCTCTTCTCCGCCTCTAAC 1684
                                                                                                                                                                                                                                                                 TGCCGTGACGTGGAGTTCATGATTGGCATCAAGACTTCGCTGTACTATCGCATCTGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTTTCTGCGCCATTTCTGAACTCGCAGGCGTGTTCTGGATTTATGGATTGGAGAATCTG 1564
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                                      DE 2 (bases 1 to 242172)

Namanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Ramann, J., Beesson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Champe, M., Dayle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Carle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nalson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D., Williams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M. Smith, H.O., Venter, J.C. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wenter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A., Welssenbach, J., Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, O.A., Ye, J., Yeh, R.F., Zaveri, J.S., Zhan, M., Zhang, G., Zhao, Q., Zheng, L., Zheng, X.H., Zhong, F.N., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C. The genome sequence of Drosophila melanogaster Science 287 (5461), 2185-2195 (2000)
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Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F.
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COMMENT
FEATURES
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AUTHORS
TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (31-MAY-2002) University of California Berkeley, Sciences Addition, Berkeley, CA 94720, USA On Jun 28, 2002 this sequence version replaced gi:10727684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-MAR-2000) Celera Genomics, 45 West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rockville, MD, USA
5 (bases 1 to 242172)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Annotation of Drosophila melanogaster genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="flybase:fbgn0050000"
/tagnslation="mskaikyyydflsqpsalmiamklgktpfedcpvalrkoeqlttytasinrqokypaiydkfolgesysivryladkoyfseqlypktleerakydefle
deyrsinrqokypaiydkfolgesysivryladkoyfseqlypktleerakydefle
mQhfnvrlvcslefrqvwllpakglapapkpesykklikdvesnlgllerlmlekdfl
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join(1614. .1731,1783. .1885,1

/gene="CG30005"
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/db_xref="FLYBASE:FBgn0050000"
/oin(334..451,527..629,694.
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                     /db_xref="FLYBASE:FBan0030005"
/db_xref="FLYBASE:FBgn0050005"
join(1548. .1731,1783. .1885,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGDKLTVADIFGSSEINQMKLCQYNVNEKQFPKVAKWMERVRDATNPYYDEAHSFVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAF58913.2"
/db_xref="GI:21627590"
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                                                                                                                 /product="CG30005-PA"
                                                                                                                                         /codon_start=1
                                                                                                                                                         'note="CG30005 gene product"
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                                                                                                                                                                                                                                                                                                     /gene="CG30005"
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                                                                                                                                                                                                                                                                                                                                                                                                                 'note-"CG12930".
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'db_xref="flyBASE:FBan0030005"
'db_xref="flyBASE:FBgn0050005"
'translation="MSKPIREYYDLLSPIARGLWIGLKFSNSPVEYCPIALRKFEQLT
                                                                      protein_id="AAM68787.1"
'db_xref="GI:21627591"
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n(237. .451,527. .629,694. .1010,1072. .1425)
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                                                                                                                                                                                        TTCTGCGCGAGAAGGCGAGCATCGATGATGGCATCGGATATCCCCAGCTGGAGCCTGGCGC 190900
                                                                                                                                                                                                                    TTCTCCAACAAAGCGATGGAATTGAAGGAGGTCTCGGTGCCCCCCATCTGGGTACTTGGTGT 779
              CGGGCAAGGCCTCCTACTTCCTCGCCCTCTTTCCCTACGTGGTGATGCTGGTGCTCCTGG 191020
                                                      CCGGCAAAGCGGCCTACTTCCTCGCGCTCTTCCCATACGTTGTCATGATCACTTTATTCA 899
                                                                                                   TGGCACTGGCTGTGGCCTGGATCGTCATCGCGGGGATTATGTTCAAGGGTGTGAAGAGTT
                                                                                                                                                                                                                                                                                    Conservative
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0,

409;

Indels

55;

Gaps

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/db_xref="FLYBASE:FBan0012926" /db_xref="FLYBASE:FBgn0033437" /db_xref="FLYBASE:FBgn0033437" complement(join(2374. .2850,2912.4387. .4531))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FLYBASE:FBan0001794"
/db_xref="FLYBASE:FBan00033438"
/db_xref="FLYBASE:FBgn0033438"
complement(join(6339. 6865,6935. .7076,7141. .8006,
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37452. .37723,51841. .51987,55619. .55840,56435. .56565,
61636. .61814,61920. .62021,77030. .77178,77521. .78096,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mseaysnsirslspelakkahdelgeipdridedietlatwisk ophikarodagelvarelrgckyslektrikkldneyambadvelknirtvbekolsis dtgcllrlpoploadgerihisrygovdskkyslaevovntwigeiogirbeddnamis geveiidmkgvgaghleoedavivkklavlgdkaypyrekgefhevnapssaekemsia kslmsekirkrehihskldslykyvpreclpaeyggsmgtiodvvstwrtkllavkpe
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/db_xref="FLYBASE:FBgn0033437"
complement(join(2596. .2850,291
/gene="CG12926"
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WQHLNIRLACSMYFRDAWLFPMNGIAPKPKPEQIQALIEGVENNLGLLERLWLENDFL
VGKNLTMADILGSSEINQLSYLN"
                                                                                                                                                                                                                                                                                                                                                           /db_xref="FLYBASE:FBan0001794"
/db_xref="FLYBASE:FBan0001794"
/db_xref="FLYBASE:FBgn0033438"
complement(join(6339. .6865,6935. .7076,7141. .8006,9074. .9219,9610. .9750,31720. .31914,35811. .36004,9074. .9219,9610. .9750,31720. .31914,35811. .36004,37452. .37723,51841. .51987,55619. .55840,56435. .56565,61636. .61814,61920. .62009))
/gene="CGI794"
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/gene="CG1794"
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/qene="CG12926"
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/gene="CG1794"
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/db_xref="GI:730366"
/db_xref="FLYBASE:FBan0012926"
/db_xref="FLYBASE:FBgn0033437"
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/gene="CG12926"
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                                                                                                               TARLIQKPRCGVGDRRSADSFSPDNLYHEIGSNVRVRRFALQGPKCCGRTEFEPSNPR
                                                                                                                                      /db_xref="FLYBASE:FBan0001794"
/db_xref="FLYBASE:FBan0033438"
/translation="MQFDYLPKSDLETGALRTEDQLKEAIRSLQSFGNITVTGEIDSA
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                                                                                                                                                                                                                                                  protein_id="AAF58911.3"
                                                                                                                                                                                                                                                                               /product="CG1794-PA"
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                          9.6%;
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Score 274.6; DB 3
Pred. No. 3.2e-49;
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 AC018319:1 GI:6552872
HTG; HTGS_PHASE2.
Drosophila melanogaster.
Drosophila melanogaster
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
                                                                                         Pieces.
AC018319
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This sequence was identified as CDM:10214336 by the submitter. For more information on this record e-mail to fly@celera.com.*
NOTE: This is a 'working draft' sequence.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Adams, M. and Venter, J.C.
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                                                                                                                                                                                   CATACCCTGATGCCATTGCCAAA----ACATTCCAACCTCAGCTATTCTCGGTGCTGTTCT 1292
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                               CCGTGCTCAAAGATCAGTTCGTGAACGTCAAGCTGTGGATTATAGTGGTCAGCCTTTCGG
                                                              CATTGGCGATGGACGCGTTCCCACGTGTACCCACCGTCTACATGTCAGCGATGACCTGTT
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3897 c 3763 g 5202 t
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ALIGNMENTS

Drosophila melanogaster expressed polynucleotide SEQ ID NO 4001.

ABL03173;

26-MAR-2002 (first entry)

ABL03173 standard; cDNA; 1956 BP

RESULT 1
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DTOS WPI; 2001-656860/75. P-PSDB; ABB59070. 23-MAR-2000; 2000US-191637P 11-JUL-2000; 2000US-0614150 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss. New isolated nucleic acid detection reagent for detecting 1000 or more Venter JC, 23-MAR-2001; 2001WO-US09231 27-SEP-2001 WO200171042-A2 Drosophila melanogaster. (PEKE) PE CORP NY. Adams M, Li PWD, Myers ¥

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(ABB57737-ABB72072).
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a Drosophila melanogaster transporter protein homologue, bloamine transporter [BT1]. The BT11s goed in screening assays to identify candidate compounds which are potential pesticide agents or therapeutics that interact with BT1 proteins. It can also be used to genetically modify metazoan invertebrate animals resulting in BT1 corposeion or research as the second in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-2001
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TTCAGTTCAAGAAACTCTGTTAAAGTTTGGTCAATTTCACCGGCCATGAAAGGTACTGGA
                                                                 GTCATCGTTCTTTTACTTGTCGGCAAGCCTGTGTACTTAGAGTGTGTCCTCGGACAA
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15-MAR-2000;
23-MAR-2000;
23-MAR-2000;
23-MAR-2000;
23-MAR-2000;
                                                                                                            Novel invertebrate symporter cell surface receptor proteins and nucleic acid encoding the protein useful as pesticide or drug target and to identify compounds that have utility as therapeutics or pesticides
                                                                                      Claim
                                                                                                                                                                                                                                                         Kellerman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fruit fly; invertebrate symporter cell surface receptor; dmKSNF;
sodium/neurotransmitter family; SNF; biopesticide; therapy;
K+ coupled amino acid transporter; ss.
                                                                                                                                                                                                                                                                                             (GENO-) GENOPTERA LLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD09681 standard;
e invention relates to invertebrate symporter cell surface receptors the sodium/neurotransmitter family (SNF) and nucleic acid molecules coding such receptors. The SNF protein is useful for detecting a
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2000US-0189399.
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C candidate compound especially a putative pesticidal or pharmaceutical agent that interacts with an invertebrate symporter cell surface receptor protein or its fragment. Insect or worm genetically modified to express protein of the invention is useful for studying invertebrate symporter cell surface receptor protein activity, by detecting the phenotype caused by the expression or mis expression of the protein or the animal. Nucleic acids encoding the invertebrate receptor protein or their fragments are useful as biopesticides. SNF nucleic acids are useful for generating mutant phenotypes in an animal model or living cells that are used to study the regulation of genes encoding the proteins which are useful as pesticide or drug targets. The genetically modified organisms or cells are useful in screening assays to identify pesticides or therapeutics and thus are useful in the identification of new drug targets, therapeutic agents, diagnostics and prognostics useful in treatment of disorders associated with ion channels. The nucleic acid molecules are also useful as hybridisation probes.

The present sequence is a cDNA encoding Drosophila melanogaster (dm) referred as amxing
reterred
as dmKSNF.
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Sequence 2473 BP; 625 A; 593 C; 627 G; 628 T; 0 other;

13.7%; 53.2%;

DB 22; Length

Query Match Best Local Similarity Matches 951; Conserv 927 867 695 755 807 643 747 **6**38 687 578 627 567 458 507 398 447 387 218 278 327 AACTCGAGGCCGCAGGAGTATGTGGACAATCTGCTTACGGGCGTATCCTTGGCCAATGAA GTCGTCGCCCGAGGAGTCAAGAGTTCCGGCAAAGCGGCCTACTTCCTCGCGCTCTTCCCA CCCTC----GGTGATCCCGATTGGAAGCTGACACTTGCCCTGTTCGTCGCCTGGGTGGTCATCTTTCTG GGTGCCCCCATCTGGTACTTGGTGTGTGTCTATTCATCGCATGGCTCATGGTGTTCGGA TCCGAACTCTATTTCCTGAATGTAGTGATCAAGGAGAAGCTGGACATCTCGGACGGCGTT GCTCAACTCTACTTTTGAGAACAGTTCTCCAACAAGCGATGGAATTGAAGGAGGTCTC TCGGCCAGAAATCTCAGCGGCATTGTGGCCAACGATGAGACAGAGAAACTCCAGAGCAGC ATGAGCTTCCAGGCCACTCTTCCATGGGCTATTTGTCAGCCTGAGTGGGAGAACTGCGTA GTGAAGATTTGGTCGGTGGTGCCGGGATTTGTGGGCGTGGGCCTATGGCCAGGCCTTCGGC GTTAAAGTTTGGTCAATTTCACCGGCCATGAAAGGTACTGGATACGCTCAAGCTGCCGGC ATCGGCAAACCCATGTACTATTTGGAGATGATCATGGGCCAGTTCACGAGCCAGGGAACG GAAAAAACAGATGCCGAGAAGCCGACGGCGGAGCGCACCAATTGGGGGCAATGGCCTGGAG 386 GTGTCCTTCCAATCGGAATTGCCGTGGTCCTACTGTCGCGATGAGTGGACCAATTGCGTG ACCATCTGCATCATCTCGTACTATTCCTCGCTGTTGGCGCTGACCCTCTACTATCTCTTT GTCGGCAAGCCTGTGTACTACTTAGAGTGTGTCCTCGGACAATTCAGTTCAAGAAACTCT ACGGCCTATGAGAATGGAGGAGGCGCCTTCCTTATACCCCTACATCATAGTGCTCTTTCTG ATCGCGTACCAGAATGGAGGAGGTGCTTTCCTGGTGCCATACGTCATCGTTCTTTTACTT 397 TTTCTAATGTCCTGCATATCGGTGTCCGTGGGATTGGGCAACGTCTGGAGGTTCCCGTTC TTCTTGATGTCCTGCATCGCTACATCCGTCGGTTTGGGTAACGTGTGGCGGTTCCCTTTC GATGACACGGACTTAGAGGCTGAACCGCCAGAACGTATGGTATGGTCCAACAACATTGAA 277 -----AGATCCAACACTTGCTGCATCAGTCAACAACATCACCAATGGTACCAGCAGT Conservative 0; Score 391.8; DB 22; Pred. No. 4.7e-76; 0; Mismatches 767; Indels 69; ----Gaps 754 694 457 926 866 806 746 637 577 626 517 566 446 642 989

GTGATCATGCGAGGGGTGAAGAGTTCCGGCAAGGCGGCCTACTTCCTGGCCCTGTTCCCC

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Matches 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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P-PSDB; ABB61784.
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melanogaster expressed polynucleotide SEQ

Drosophila; developmental pharmaceutical; gene; ss. biology; cell signalling; insecticide;

Drosophila melanogaster

WO200171042

27-SEP-2001

23-MAR-2001; 2001WO-US09231

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23-MAR-2000; 11-JUL-2000; 2000US-191637P 2000US-0614150

(PEKE) PE CORP NY.

JС, Adams M, Ŀi PWD, Myers Æ

P-PSDB; 2001-656860/75 DB; ABB63648.

New isolated nucleic agenes from Drosophila interactions e acid detection reagent for detecting for elucidating cell signalling 1000 and (cell-cell

Claim SEQ ID NO 17735; 21pp + Sequence Listing; English

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention is

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Matches 788
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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sodium/neurotransmitter family; SNF; biopesticide; therapy;
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The invention relates to invertebrate symporter cell surface receptors CC of the sodium/neurotransmitter family (SNF) and nucleic acid molecules encoding such receptors. The SNF protein is useful for detecting a CC candidate compound especially a putative pesticidal or pharmaceutical agent that interacts with an invertebrate symporter cell surface receptor protein or its fragment. Insect or worm genetically modified CC receptor protein or it fragment. Insect or worm genetically modified CC express protein of the invention is useful for studying invertebrate symporter cell surface receptor protein activity, by detecting the phenotype caused by the expression or mis-expression of the protein or the animal. Nucleic acids encoding the invertebrate receptor protein or the animal sucleic acids encoding the invertebrate receptor protein or their fragments are useful as biopesticides. SNF nucleic acids are useful for generating mutant phenotypes in an animal model or living cells that are useful as pesticide or drug targets. The genetically modified organisms or cells are useful in screening assays to identify cesticides or therapeutics and thus are useful in the identification of new drug targets, therapeutic agents, diagnostics and prognostics concleic acid molecules are also useful as hybridisation probes.

CC nucleic acid molecules are also useful as hybridisation probes.
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developmental biology; cell signalling;
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Matches 976;
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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15-MAR-2000;
23-MAR-2000;
                  The invention relates to invertebrate symporter cell surface receptor of the sodium/neurotransmitter family (SNF) and nucleic acid molecule encoding such receptors. The SNF protein is useful for detecting a candidate compound especially a putative pesticidal or pharmaceutical agent that interacts with an invertebrate symporter cell surface
                                                                                                                                                                                 Novel invertebrate symporter cell surface receptor proteins and nucleic acid encoding the protein useful as pesticide or drug target and to identify compounds that have utility as therapeutics or pesticides -
                                                                                                                                                    Claim 5; Page 67;
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The present sequence is a cDNA encoding Drosophila melanogaster (dm)
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                                                                                 TGGAATTGGATTTTCTTTGTACAAATACCGTACCGGAACCTTCAGCGAGACGATCAAGAA
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                                                     TTGGATGATCGTGGCCATTGTTCGAGATCCAGGTCAGACTTTGGGTGCAAAAATCCGTGG
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Matches 595
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and interactions -
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P-PSDB; ABB59069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO
                 TGCGGGCACTCACCTTGCCGGGCGCCTTCGACGGCGTGCTGTACTTCCTGCGGCCGCAAT
                                TCACCACAATCATCCTGCCCGGTGCTACTGACGGCATCCTGTTCTTCGTCACGCCTCAAT
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detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell

Sequence Listing;

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Score 274.6; DB 23; Pred. No. 2.7e-50; 0; Mismatches 409;

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ABL03172 standard; cDNA;
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                                                                                                                                                   Drosophila melanogaster
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2000US-0614150
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Myers
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RESULT 11
ABL07750/c
ID ABL07750 standard; cDNA; 4385 BP
XX
AC ABL07750;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expresse
XX
KW Drosophila; developmental biolog
KW pharmaceutical; gene; ss.
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OS Drosophila melanogaster.
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PN W0200171042-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of specification, but was obtained in electronic format di at ftp.wipo.int/pub/published_pct_sequences.
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(ABB57737-ABB72072)
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11-JUL-2000;
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                                             CATTCACCTCACTGCTCTCGGGTGTGATTATCTTTGGAATCCTGGGAAACCTGGCTCACG
                                                              CCTTTACAAGTTTCTTGTCTGGGTGCACGATCTTCGGTATCCTTGGTAACCTCGCGTACG
                                                                                                                       CTTACAACGGTTTCAGACATAATATCTACAGGGATGCTTGGATTGTTACGACTTTGGACA 1115
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The sequence data for the development of sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                            New isolated nucleic acid
genes from Drosophila and
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specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
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TACTCAGCAGTCACGCAAGTGTTCTTCTCTCTGACAGTGTGCACCGGACCGATCATCATG CAGGGAATTGTGTACTTCCTGAAGCCCCAATGGTCCCAGCTGCTCAATCCGCACGTGTGG GACGGCATCCTGTTCTTCGTCACGCCTCAATGGGCGAAACTCCTTGAGCTCGGTGTATGG TTTCCCTATGTGATCATGATCGTACTGCTCATTCGGGCGGTCACTTTACCAGGTGCCTGG GCACGATTTTGTCAAAGGGCATTCGCAGTTCTGGGAAAGCTTCCTATTTCCTGGCCCTG GGCCTGGGTACTCCCAGTTGGGATCTGGTCTTGTTCTCTGGCCACTTGGGTGATCATC GGTCTCGGTGCCCCCATCTGGTACTTGGTGTTGTGTCTATTCATCGCATGGCTCATGGTG TTCTCCTCTTACAACGGTTTCAGACATAAT---TACGCGGCCATCACACAGATGTTCTTCTCGCTGGCCATCTGCTTCGGAACGCTGGTCATG TTCCCATACGTTGTCATGATCACCTTTATTCATCACCACAATCATCCTGCCCGGTGCTACT TTCGGAGTCGTCGCCCGAGGAGTCAAGAGTTCCGGCCAAAGCGGCCTACTTCCTCGCGCTC -----ATCTACAGGGATGCTTGGATTGTTACGACTTTGG 0; Score 247.4; DB 2 Pred. No. 2.6e-44; D; Mismatches 391 Indels 59; Gaps 3351 1112 3291 1048 3171 3111 2991 1078 3231 928 868

TTGAGACCAACACCAAGGATATTTCGCAGGTTGTCAAAGGTGGAGCTGGTCTAGCGTTCA ACGAACTCAACTCAGAGGTGGGAGATGTGGGGGGTGCTGGCGGTACCAGTCTTTCA ACTCGCTTACATCCATTCTGGCTGGTTGCATCATCTTTGGAATTCTGGGCAACCTGGCCT ACACCTTTACAAGTTTCTTGTCTGGGTGCACGATCTTCGGTATCCTTGGTAACCTCGCGT TTTCAGATCATCTTTATGTGTCATTCCTTTCCAGAGATGTGATAATAATCACCACTATAG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - \,
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[ABB57737-ABB72072].
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                                   The present sequence represents the nucleotide sequence of rat glycine transporter 2 (rGly7-2), for use in the present invention. The present invention describes a non-mammalian cell comprising an exogenous nucleic acid sequence encoding a glycine transporter. The invention also describes screening for an enhancer or inhibitor of glycine transporter. The enhancer/inhibitor can be used to treat pain, spasticity, myoclonus, muscle spasm or hyperactivity, epilepsy, stroke, head trauma, neuronal cell death, spinal cord injury, dystonia, Alzheimer's, Parkinson's or Huntington's disease, multi-infarct or AIDS dementia, multiple or amyotrophic lateral sclerosis, attention deficit disorder, organic brain syndromes, schizophrenia or memory or cognitive
Sequence
                                                                                                                                                                                                Claim 9;
                                                                                                                                                                                                                                  Non-mammalian cell comprising exogenous glycine transporter DNA for screening for glycine transporter enhancer or inhibitor, e. treat Alzheimer's, Parkinson's or Huntington's disease or AIDS
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htt genomic AE03832: arm:2R [4615216,4876965]
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AT.121-AT.319: DH5-alpha TonA"
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/clone_lib="AT Drosophila melanogaster adult testes
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Email: HoltRA@celera.com Plate: NU01004ABO row: O
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Tel: 2404533151
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Db 623 CTGGCCCTCTTCCCGTACGTCGTGCTGATCTGCTCACGCCAATCACCTTCACGCTGGAG 564	683 GTGGCGATGACMATCATGATGGTGAAGGGTATCCGGCGATGCCGCAAGGTCGCATAYTTT		Db 743 ACTGCGGGTGCTGGGTGCCGGACTGGGRAASTRACGCTCTGCTGTCTTMATCTG 684	Best Local Similarity 54.8%; Pred. No. 8.9e-17; Matches 311; Conservative 5; Mismatches 249; Indels 3; Gaps	Watch 5.3%: Score 151 6: DR 17.	/clone="19M22" /clone_lib="MotreDame1" /note="end : SP6" BASE COUNT 194 a 209 c 217 g 145 t 12 others	/organism="Anopheles gambiae" /strain="pBST" /db_xref="taxoo:7165"	ц н	Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur	AL Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue Roux, Paris 75015, France		<pre>- FRANCE (E-mail : seqref@genoscope.cns. ns.fr)</pre>	AUTHORS Genoscope. TITLE Direct Submission JOURNAL Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :	Anopheles. 1 (bases 1 to 777)	Eukaryota Neoptera;	MS	VERSOLUM AL149994 VERSOLUM AL149894.1 GI:7010373 KEYWORDS GSS	genomic survey sequence.	DEFINITION Anopheles gambiae GSS SP6 end of clone 19M22 of NotreDamel library	T 3 LOL/C CNEGITAL	Db 689 CATCAT 694	Qy 880 TGTCAT 885 .	629 GATCAAAGGCATTAAGAGCTCCGGCAAGGTTTCGTACTTCCCTTGCCATCTTCCCGTACAT	Qy 820 CGCCCGAGGAGTCAAGAGTTCCGGCAAAGCGGCCTACTTCCTCGCGCTCTTCCCCATACGT 879	Qy 760 CCCCATCTGGTACTTGGTGTTCTGTGTCTATTCATCGCATGGTCTCTTCGGAGTCGT 819 III III III IIII IIII IIII IIII IIIII IIIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 509 TCTGTACTTCCGCAAAACGGTAATGCATGCCGCTGACTCACTGGACGATGGGTTGGGATA 568	700
source	FEATURES					•	REMARK COMMENT		AUTHORS TITLE JOURNAL	REFERENCE	ORGANISM	VERSION KEYWORDS	DEFINITION	BC026339 LOCUS		Db	Qy	Db	Qy .	Db Qy	Db	Qy		Ov	Qy Db	Db	Qу
	passed the following selection criteria: matched mRNA g1: 4 This clone has the following problem: frame shifted. Location/Qualifiers	IRAK Plate: 32 Row: d Column: 18 one was selected for full length sequenci	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305		NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Fmail: Graphe-Gmail th Cor	<pre>Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA</pre>	Strausberg, R. Direct Submission Submitted (02-APR-2002) National Institutes of	Mammalia, Eutheria, Primates; Catarrhini; Hominidae	Homo sapiens Fukarvota: Metagoa: Chordata:		Homo sapiens, solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12, clone IMAGE:47943	BC026339 3118 hp mpNA linear H™C 08-App-2002		203 TICGCGCTGCTTCTTCATGCTGT 176	1277 TICTCGGTGCTGTTCTTCCTGATGATGT 1304	263 GGCCTAACGTTCATCACCTACCCCGATGCGCTGGCCAAGTTTGAGCACGTCCCGAACCTG 204	1220 AGTCTTGCTTTCATTTCATACCCTGATGCCATTGCCAAAACATTCCAACCTCAGCTA 1276	1160 GGTAACCTCGCGTACGAACTCAACTCAGAGGTGGGAGATGTGGTCGGTGCTGGCGGTACC 1219	383 ATCTCGTGGATACGTTCACCTCCCTACTCTCCGGGGGCCTCGTGTTCTCCATCATT 324	CTTTACAAGTTTCTTGTCTGGGTGCACGATC	GTCATTGCCTTCTACAACAACTTCAGCAACAATATTTACCGGGATGCGATGATCATCA	1040 ATCATCATCTTCTTCTTCTTTACAACACACACACACACA	980 GGTGTATGGTACTCAGCAGTCACGCAAGTGTTCTCTCTCT	ACCCGÁC	920 GGTGCTACTGACGGCATCCTGTTCTTCGTCACGCCTCAATGGGCGAAACTCCTTGAGCTC 979

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oution information can be found WL at: http://image.llnl.gov . 18
                                                                                                          E. Consortium (LLNL) at the Stanford Human Genome feedicine, Stanford, CA 94305 ford.edu
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TTGGACACCTTTACAAGTTTCTTGTCTGGGTGCACGATCTTCGGTATCCTTGGTAACCTC
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                                                                                                                                                             GACGGCATCCTGTTCTTCGTCACGCCTCAATGGGCGAAACTCCTTGAGCTCGGTGTATGG.
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                                                       TTCTCCTCTTACAACGGTTTCAGACATAATATCTACAGGGATGCTTGGATTGTTACGACT
                                                                                    ATGGATGCGGGCACCCAGATCTTCTTCTTCTTTGCCATCTGCCAGGGGTGCCTGACAGCC
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/tissue_type="Brain, hypothalamus"
/clone_lib="NHL MGC_96"
/lab_host="DH108"
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/note="Vector: pBluescript"
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D; Mismatches 814;
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21384984
Contact: Ettensohn CA
Dept. Biol. Sci.
Carnegie Mellon University
4400 Fifth Avenue, Pittsburgh,
                                                                                                                                             Strongylocentrotus purpuratus.
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodemata; Eleutherozoa;
Echinoidea; Euchinoidea; Echinoidea;
Strongylocentrotidae; Strongylocentrotus.

1 (bases 1 to 798)
                                                                         Ettensohn,C.A.
A large scale analysis of mRNAs cells of the sea urchin embryo Development 128 (13), 2615-2627
                                                                                                                                     Zhu, X., Mahairas, G., Illies, M.R.,
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                                                                           CTTGTGCTTTTTCTGCGCCATTTTCTGAACTCGCAGGCGTGTTCTGGATTTATGGA 1552
                                                                                                                             TACTGCACACCGGGTGGACAATATTTCTTGAGCTTGTAGATCACTACGGTGGAACATTC 1498
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                                                             TCCCTCATTATGTTCGGCCTTTGCGAGACCATTGGCCTCTCCTGGTTCTATGGA
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/db_xref="taxon:7668"
/clone="91222951_N20_072_PC_0020_B2_MR_G10"
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/lab_host="E.coli"
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Query Match
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On Dec 6, 2000 this sequence version
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On Dec 6, 2000 this sequence version
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Plate: AT.204 row: A column: 11
High quality sequence stop: 565.
Location/Qualifiers
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hit genomic AE003434: arm:X [5132852,5435637]
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ilarity 58.4%;
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/db_xref="taxon:7227"
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Berkeley, CA 94720,
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Pred. No. 4.8e-15;
0; Mismatches 177;
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363

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BASE COUNT
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1 (bases 1 to 802)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurola
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1884725 802 bp mRNA linear EST 07-MAR-2000 w183h06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431547 3/ similar to SW:NTGL_HUMAN P48067 SODIUM- AND CHLORIDE-DEPENDENT GLYCINE TRANSPORTER 1 ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-GGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: David N. Louis, M.D., Myrna R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
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                                                                                     Similarity
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Insert Length: 1128 Std Error: 0.00
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n quality sequence stop: 464.
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                                                                                                                                                             adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

1 222 c 240 g 145 t 1 others
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                                                                                 4.98;
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Primates;
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                                                                                 Score 139.4; DB 9
Pred. No. 1.2e-14;
                                                                Mismatches
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                                                                                                    DB 9;
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                                                                                                                                                                              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
IMPORTANT: this sequence may contain errors. The Ciona intestinalis
Library from which the clone was isolated may be contaminated with
cDNAs from bacteria or other Eukarya.
Directional larval cDNA library originate from Dr.M.Branno,
Stazione A.Dohrn, Naples, Italy, and was prepared in
                                                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope.
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Ciona intestinalis
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/clone="021ZF11"
/clone_lib="directional larval cDNA library"
/note="Vector: pBluescript2SK+"
/note="Vector: pBluescript2SK+"
/note="171 c 197 g 277 t 2 others
                                                                              /organism="Ciona intestinalis"
/db_xref="taxon:7719"
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Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
                                                                                 Mita,K., Morimyo,M., Shimada,T., Okano,K. and Establishment of cDNA database of Bombyx mori Unpublished (1999)
                                                                                                                                                                                                                                                   AU002272
AU002272.1
                                                                                                                                                                                                                                                                                                  AU002272 499 bp
AU002272 Bombyx mori p50(Daizo)
                                                                     Contact: Mita K
                                                                                                                                 Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 499)
                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
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                                                                                                                                                                                                                  domestic silkworm.
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                 JOURNAI
                                                AUTHORS
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                             Direct Submission
Submitted (01-0CT-2001) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
2 (hases 1 to 527)
Roth.C.W., Brey,F.T., Ke,Z. and Collins,F.H.
Direct Submission
                                                                                                                                                                                   Anopheles gambiae
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Alptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                           CNS07HXH

527 bp DNA linear GSS 03-OCT-200
Anopheles gambiae GSS SP6 end of clone 31F21 of library NotreDame1
from strain PEST of Anopheles gambiae (African malaria mosquito),
Submitted (01-OCT-2001) BBMI, Roux, Paris 75015, France
                                                                                                                                               Genoscope.
                                                                                                                                                             Anopheles.
1 (bases 1 to 527)
                                                                                                                                                                                                                                                                                                              genomic survey sequence.
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/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="mg0698"
/clone_lib="Bombyx mori p'
/clone_lib="Bombyx mori p'
a 91 c 107 g 156
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Location/Qualifiers
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Pred. No. 2.2e-13;
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COMMENT
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AUTHORS
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Unpublished (2001)
On Dec 1, 1998 this sequence
Other_ESTs: GH16161.3prime
                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 811)
                                                Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                   AI293077

811 bp mRNA linear EST 23-APR-2001 GH16161.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH16161 5 similar to BG:DS03431.1: FBan0015279 located on: 2L 35B7-35B7;: 04/10/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is from an A. gambiae BAC library provided by F.H Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.
                                                                                                                                                                                                                         AI293077.2
                                                                                                                                                                                         fruit fly.
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/strain="pEST"
/db xref="taxon:7165"
/clone="31F21"
/clone_11b="NotreDame1"
/note="end : Sp6"
a 157 c 138 g 14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003645: arm:2L [14622887,14883853]
estimated-cyto:3585-3589: 04/10/2001
plate: GH.161 row: F column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence Berkeley One Cyclotron Rd, Fax: 510 486 6798
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                                                                  TATC
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                                                                                                                                    ATATTTCATTGAATCATTTCGCAACCCATTGCCCTGGTCCACATGCCGTGCGGAATGGGG
                                                                                                                                                   TTACTTAGCTATGAGCTTCCAGGCCACTCTTCCATGGGCTATTTGTCAGCCTGAGTGGGA 627
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                                                                                                                                                                                                    GGCTTTCCAGGTGTTCATGCTCAGCACTTACTATGCCGCCCTGGTAGCGATAATTGGCCG
                                                                                                                                                                                                                                   AAGAAACTCTGTTAAAGTTTGGTCAATTTCACCGGCCATGAAAGGTACTGGATACGCTCA 507
                                                                                                                                                                                                                                                                                                                                      CCTGTTCCTGATTGGCAAACCGATTTACTATCTGGAAATGGTAATTGGCCAGTTTTCCAG 382
                                                                                                                                                                                                                                                                                                                                                                                                        ATTCCCCTTTACTGCCCTCGATAATGGCGGTGGCGCCTTCCTCATACCATATCTCATTGT
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                                                                                                                                                                                                                                                                    TCGGGGCTCGGTTAAAGTGTTCGATTTGTGCCCCGGCGATGAAAGGTGTTGGAGCTGGCCA 442
                                                                                                                                                                                                                                                                                                                                                                     TCTTTTACTTGTCGGCAAGCCTGTGTACTACTTAGAGTGTGTCCTCGGACAATTCAGTTC
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/note="Organ; head; Vector: pOT
/note; Sized fractionated cDNAs
XhoI; Sized fractionated cDNAs
pOT2. plasmid cDNA library."
199 c 214 g 202 t
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/sex="male and female"
/dev_stage="adult"
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/db_xref="taxon:7227"
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Berkeley, CA.94720,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel
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                                                                                        GATCATCATCTTCTTCTTACAACGGTTTCAGACATAATATCTACAGGGATGCTTGGAT 1098
                                                                                                                                                                                                                                    CGGTGCTACTGACGGCATCCTGTTCTTCGTCACGCCTCAATGGGCGAAACTCCTTGAGCT
                                                                                                                                                                                                                                                                                                            CCTCGCGCTCTTCCCCATACGTTGTCATGATCACTTTATTCATCACCACAATCATCCTGCC
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                                                                                                                                                                                                                                                                                                                                                                     CTCATGGTGTTCGGAGTCGTCGCCCGAGGGAGTTCAAGAGTTCCGGCAAAGCGGCCTACTT
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                                                    AATCATTGCGTACTCCTCGTTCAATAATTTCTCCCAATAATGTCTATCGTGATGCAATGAT
                                                                                                                            CAAGGTATGGATGGAAGCAGTCACACAGTGTTTCTTCTCCCTGTCAATCTGTTTTGGTGG
                                                                                                                                                            CGGTGTATGGTACTCAGCAGTCACGCAAGTGTTCTTCTCTCTGACAGTGTGCACCGGACC 1038
                                                                                                                                                                                                  AGGTTCGCTCGAGGGTATCAAGTTCTTCCTAACCCCCAAATGGGAAAGCCTATTCTCAGC 574
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1: 2404533151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HoltRA@celera.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
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/strain="RSP-ST (Reduced susc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="A.Gam.ad.cDNA1"
/dev_stage="Adult"
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Pred. No. 2.2e-12;
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Unpublished (2002)
Contact: Holt R.A.
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17000687244048 A.Gam.ad.cDNA.bloodl Anopheles
19600449683580 5', mRNA sequence.
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Fax: 2404534580
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45 w. Gude Dr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holt, R.A., Lin, J.-J.,
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Seq primer: M13 Reverse.
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R.
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                                                                                                                            ACCTCAGCTATTCTCGGTGCTGTTCTTCCTGATGATGTGGCTGGGTGTGGGTATCGGCTCATC 1326
                                                                                                                                                                                                                 TGGCGGTACCAGTCTTGCTTTCATTCATACCCTGATGCCATTGCCAA---AACATTCCA 1266
                                                                                                                                                                                                                                                                                         CGGTATCCTTGGTAACCTCGCGTACGAACTCAACTCAGAGGTGGGAGATGTGGTCGGTGC 1209
                                                                                                                                                                                                                                                                                                                             TGCGCTGATCATAACCTCACTCGACACTGTCACTTCGCTGGTGGCCGGGTGCGTTGTGTT
                                                                                                                                                                                                                                                                                                                                                               TGCTTGGATTGTTACGACTTTGGACACCTTTACAAGTTTCTTGTCTGGGTGCACGATCTT 1149
                                                                                                                                                                                                                                                                                                                                                                                                     CACGCGTCCGCTGATCGTATATTCGTCCTTTAACGACTTCTCCAACAACATCTACCGCCA
CGTCTACATGTCAGCGATGACCTGTTCTTGCGGTTTCCTGCTTGGACTTGTTTACTGCAC
                                   GATCGGTATCGTAACGTCCGTGATTACCGCCATCCACGACCAGCGGCCGGACATTGCGCG
                                                                     CGTGGCTCTGCTATCGACTTTCAACACATTGGCGATGGACGCGTTCCCCACGTGTACCCAC 1386
                                                                                                         GCCGCAGTTCTTCGGCTGCTATTCTTCATCATGCTGCTCCTCGCCATTGGTACGCT 302
                                                                                                                                                                                                                                                     CGGTGTGATTGGTCATCTAGCTCACGTCACCGGTCAGTCGGACATCTCCAAAGTCGTCCA 182
                                                                                                                                                                                 AAGTGGCCCAGCCCTTACCTTCATCACCCTACCCGGACACGATCGCCAAGTTTGACTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collins, F.H., Venter, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HoltRA@celera.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pSport1; Site_1: Sall; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDnA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)" a 173 c 150 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="19600449683580"
/clone_lib="A.Gam.ad.cDNA.blood1"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Anopheles gambiae"
/strain="RSP-ST (Reduced susc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10b"
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Pred. No. 4.5e-12;
Vismatches 272;
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Culicoidea;
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Gaps

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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library preparation: Dr. M. Bento Soares, Univeristy of CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: MGC clone distribution information can if found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTAGACATTGAGTTCATGTTGGGTAAAAAGACTGG 1602
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                                                                        134
                                                          /tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="pH10B (TI phage resistant)"
/lab_host="pH10B (TI phage resistant)"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
, is CAGCCACGAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Instututes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

34 a 233 c 193 g 215 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:5698664"
/clone_11b="NIH_BMAP_EQO"
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Rodentia;
    Score 121.4;
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                                                                                                                                                                                              genomic survey sequence.
AL157191
AL157191.1 GI:7018110
                                                                                                                                                                                                                                                             CNS01RBB 584 bp DNA linear GSS 14-JUN-200 Anopheles gambiae GSS T7 end of clone 32L10 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                              GSS
                       Genoscope.
                                                                   Anopheles.
                                                                                   Neoptera; Endopterygota;
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                                                                                                                               Anopheles gambiae
                                                                                                                                                    African malaria mosquito.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGTTTGCCGGATTCGTCATCTTCTCCATCGTGGGCTTCATGGCTCATGTCACCAAGAG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTGTTCTTCTCTGACAGTGTGCACCGGACCGATCATCATGTTCTCCTCTTACAACGG 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTCACGCCTCAATGGGCGAAACTCCTTGAGCTCGGTGTATGGTACTCAGCAGTCACGCA 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTGTTGGTTGGACTGGAAAGGTGGTCTACTTCTCAGCCACGTACCCCTACATCATGCT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTACCTGATTGGCCTGTCTAACATCACCCAAGGTGGCATTTATGTCTTCANACTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCGTTCCCACGTGTACCCCACCGTCTACATG-----TCAGCGATGACCTGTTCTTGCGG 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTGTGACACAGCTACCCATCTCCCCCTCTGGGCTATCCTCTTCTTCTCCATGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCATAGCTGATGTGGCAGCCTCAGGC----CCGGGGCCTGGCATTCTTGGCGTACCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGGTGGGAGATGTGGTCGGTGCTGGCGGTACCAGTCTTGCTTTCATTTCATACCCTGA 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCCACAACAATGTGTACAGGGACTCCATCATCGTTTGCTGCATCAACTCCTGCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTCAGACATAATATCTACAGGGATGCTTGGATTGTTACGACTTTGGACACCTTTACAAG 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCACACCCAACTTCCGAAAGCTGTCTGATTCTGAGGTGTGGCTTGACGCCGCCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGAGTCAAGAGTTCCGGCAAAGCGGCCTACTTCCTCGCGCTCTTCCCATACGTTGTCAT 885
                                       (bases 1 to 584)
                                                                                                        Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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); Mismatches 348;
                                                                                      Diptera;
                                                                                      Nematocera; Culicoidea
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GSS 14-JUN-2001

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TITLE
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Best Local Similarity 52.8%;
Matches 274; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                 1159
                          1219 CAGTCTTGCTTTCATTTCATACCCTGATGCCATTGCCAA 1257
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                                                                                                                                                                                                    1099 TGTTACGACTTTGGACACCTTTACAAGTTTCTTGTCTGGGTGCACGATCTTCGGTATCCT 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ACTGCGGGCGAGTCCGGCGTGCCGGACTGGAAGCTGACGCYCTGCCTGCYCTTCATCKGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web: www.genoscope.cns.fr)

2 (bases 1 to 584)

Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.

Direct Submission

Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.

Roux, Paris 75015, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteur.
                                                                                                                                                            CATCTCGTGGCTGGATACGTTCACCTCCCTACTCTCCGGGGCGCTCGTGTTCTCCATCAT 479
TGGCCTAACGTTCATCACCTACCCCGATGCGCCTGGCCAA 578
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                                                                          TGGCCATCTGGGACATCTGACAAACGAAACCGACTACACCAAGGTGGTAAAGCCGGGCAG 539
                                                                                                                  TGGTAACCTCGCGTACGAACTCAACTCAGAGGTGGGAGATGTGGTCGGTGCTGGCGGTAC 1218
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/strain="PEST"
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/clone="32L10"
/clone_lib="NotreDame1"
/note="end: T7"
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Search completed: July 26, 2003, 03:07:04 Job time: 3907 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Result
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Listing first 45 summaries
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US-07-879-617A-7
US-08-753-985-7
US-08-301-722A-1
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US-09-795-943-10
US-08-834-467-1
US-09-020-753-1
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PCT-US93-01959-1	US-09-343-361-1	US-08-295-814E-1	US-09-191-468-71	PCT-US92-09662-1	US-09-084-813-1	US-08-240-783B-1	PCT-US95-10579-1	PCT-US94-00119-1	US-08-291-299-1	US-08-543-881-1	PCT-US93-01959-3	US-09-343-361-3	US-08-295-814E-3	PCT-US93-01959-9	US-09-343-361-9	US-08-295-814E-9	us-09-020-753-3
Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 71, Appl	Sequence 1, Appli	Sequence 1, Appli	,-	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli		•	Sequence 9, Appli	Sequence 9, Appli	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-08-700-013B-26
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TOPOLOGY:
US-08-700-013B-26
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Query Match
Best Local Similarity
Matches 503; Conserv
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                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Albert, Vivian R.
APPLICANT: Kowalski, Leslie R.Z.
APPLICANT: Borden, Laurence A.
APPLICANT: MCKelvy, Jeffrey F.
TITLE OF INVENTION: Human Glycin
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: 1
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                             TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                             NAME: Bloom, Allen REGISTRATION NUMBER: 29,135
                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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997 Lenox Drive, Building
       Conservative
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                       54.1%;
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                                       7.8%;
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     Score 222; DB 2;
Pred. No. 1.1e-44;
D; Mismatches 415
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                                     Length 2403;
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RESULT 2
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              Sequence 4, Application U
Patent No. 5824486
GENERAL INFORMATION:
APPLICANT: Borden, La
APPLICANT: De Vivo, N
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 Borden, Laurence
De Vivo, Michael
Yokoyama, Midori
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US-08-655-836-4
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REFERENCE/DOCKET NUMBER: 3177
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEPHONE: 609-520-3259
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2817 base pairs
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Best Local S
Matches 503
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenting Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,836
FILING DATE: 31-MAY-1996
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Albert, Vivian R.
TITLE OF INVENTION: GLYCINE TRANSPORTER-TRANSFECTED CELLS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 503; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: doub TOPOLOGY: linear
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STATE: NJ
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                                                         CTCGCGTACGAACTCAACTCAGAGGTGGGAGATGTGGTCGGTGCTGGCGGTACCAGTCTT
                                                                                                                                                                                              ATGTTCTCCTCTTACAACGGTTTCAGACATAATATCTACAGGGATGCTTGGATTGTTACG
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GCTTTCATTTCATACCCTGATGCCATTGCCAAAACATTCCAACCTCAGCTATTCTCGGTG
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P.O. Box 5218
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ilarity 54.1%;
Conservative
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APPLICANT: Borden
APPLICANT: DeVivo
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/655,836
FILING DATE: 31-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: BLOOM, Allen
REGISTRATION NUMBER: 29/135
REFERENCE/DOCKET NUMBER: 317743-
                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yokoyama, Midori
APPLICANT: Albert, Vivian R.
TITLE OF INVENTION: Glycine Transporter-Transfected
TITLE OF INVENTION: Cells and Uses Thereof
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechart Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                           TELECOMMUNICATION INFORMATION: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                CITY: Lawr
STATE: NJ
                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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DeVivo, Michael
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Best Local Similarity
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CCGACCATTTTAACGTTTATCCTTTGCTTC 2298
                           CCTGCTATAATGACGACTGTGTTCTTCTAC
                                                           GAGATGATGATTCCAGCCCAACATTTTCTGGAAGGTCTGCTGGGCGTTTGTCACA
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Pred. No. 1.2e-44;
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; LIBRARY: rat forebrain cDNA library
; CLONE: rTB2-2-20
US-07-879-617A-7
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US-07-879-617A-7
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fremeau Jr., Robert T.
APPLICANT: Caron, Marc G.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affinity L-Proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Rati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 404-815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
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SOFTWARE: PatentI
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   TACGCTCAAGCTGCCGGCTGCGGTTACATCCTGTCTTACTACGTGGTGATCTGTGGTCTC
                                                              TTCAGTTCAAGAAACTCTGTTAAAGTTTTGGTCAATTTCACCGGCCATGAAAGGTACTGGA
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                                    TTCTCCAGCCTGGGACCCCTGGCTGTCTGGAAAATCAGCCCCCTCTTCAAAGGTGCGGGT
                                                                                                           Georgia
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SYSTEM: PC-DOS/MS-DOS
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	320 GTGTGGCGGTTCCCTTTCATCGCGTACCAGAATGGAGGAGGTGCTTTCCTGGTGCCATAC 379	Qy
1382 CCCACCGTCTACATGTCAGCGATGACCTGTTCTTGCGGTTTCCTGCTTGGA	267	Db
1322 TCATCGTGGCTCTGCTATCGACTTTCAACACATTGCGCATGGAGGGGTTCCCACGTGTA 1	TGGTCCAACAACATTGAATTCTTGATGTCCTGCATCGCTACATCCGTCGGTTTGGGTAAC	Qy
1262 TTCCAACCTCAGCTATTCTCGGTGCTGTTCTTCCTGATGATGTCGGTGCTGGTATCGGC 1	atch 7.3%; Score 209.6; DB 1; Length 2728; cal Similarity 48.2%; Pred. No. 1.2e-41; 707; Conservative 0; Mismatches 729; Indels 30; Gaps 3;	Query M Best Lo Matches
1202 GTCGGTGCTGGCGGTACCAGTCTTGCTTTCATTTCATACCCTGATGCCATTGCCAAAACA	IMMEDIATE SOURCE: Qy LIBRARY: rat forebrain cDNA library CLONE: rTB2-2-20 Db -08-753-985-7	80-sn
1142 ACGATCTTCGGTATCCTTGGTAACCTCGCGTACGAACTCAACTCAGAGGTGGGAGATGTG	ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Rattus TISSUE TYPE: Brain Db	
1082 TACAGGGATGCTTGGATTGTTACGACTTTGGACACCTTTACAAGTTTCTTGTCTGGGTGC		
1022 ACAGTGTGCACCGGACCGATCATCATGTTCTCCTCTTACAACGGTTTCAGACATAATATC	INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: SEQUENCE: 2728 base pairs TYPE: nucleic acid Db	 II
962 GCGAAACTCCTTGAGCTCGGTGTATGGTACTCAGCAGTCACGCAAGTGTTCTCTCTC	55628	
902 ACCACAATCATCCTGCCCGGTGCTACTGACGGCATCCTGTTCTTCGTCACGCCTCAATGG	Y-199 ATION a L. : 31	
842 GGCAAAGCGGCCTACTTCCTCGCGCTCTTCCCATACGTTGTCATGATCACTTTATTCATC	03-DEC- ON: 536 ION DATA: NUMBER:	
782 TGTCTATTCATCGCATGGCTCATGGTGTTCGGAGTCGCCCCGAGGAGTCAAGAGTTCC	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/753,985 Db	
722 CTCCAACAAGCGATGGAATTGAAGGAGGTCTCGGTGCCCCCATCTGGTACTTGGTGTTTG	ZIP: 30309 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: DAM PC compatible	
662 TCAGTCAACAACATCACCAATGGTACCAGCAGTGCTCAACTCTACTTTTGAGAACAGTT	100 Peachtree s anta orgia U.S.	
620 GAGTGGGAGAACTGCGTACCCTCAGATCCAACACTTGCTGCA	TITILE OF INVENTION: A High Affinity L-Proline Transporter NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: ADDRESSE: Kilpatrick & Cody Db	
560 TGTCTGTATTACTTAGCTATGAGCTTCCAGGCCACTCTTCCATGGGCTATTTGTCAGCCT	NFORMATION: NT: Fremeau Jr., Rob NT: Caron, Marc G. NT: Blakely, Randy E	; ; GE
500 TACGCTCAAGCTGCCGGCTGCGGTTACATCCTGTCTTACTACGTGGTGATCTGTGGTCTC	OBUT 5 7 985-7 Qy -08753985 Patent No. 5759788 Db	RESULT 5 US-08-753-9 ; Sequence ; Patent No
440 TTCAGTTCAAGAAACTCTGTTAAAGTTTGGTCAATTTCACCGGCCATGAAAGGTACTGGA 499		Db
328 TTCCTCATGCTGGCCATCTGTGGCATCCCCCTCTTTCTTGAGCTCTCCCTGGGCCAG 387	1585 AGGGCCTGCTGGCTGTTTTTGTCTCCGGCCACACTCTTGGCCTTGCTGGTGTACAGTATC 1644 1673 CTCGCCTCTAACAACCTGGTGTTCGG 1698	ρ β
	1525 ATCCAGGGTTTTGTGTGACATCCACATGATGCTGGGCTTCAAGCCAGGACTCTACTTC 1584 1613 CGTCTCTGGGGGCGTAATCACTCCTGCTATAATGACGACTGTGTTCTTCTACGCTCTT 1672	Qy
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Patent No. 5312734
GENERAL INFORMATION:
                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                            NAME: Murphy, Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0: FILING DATE: 19910920 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Murphy, Gerald M.
                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Birch, Stewart, Kolasch & Birch
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                  IMMEDIATE SOURCE:
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                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                      ORGANISM:
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Lin, Chien-Liang
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Shimada, Shoichi
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US-08-301-722A-1
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GENERAL INFORMATION:
                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Vandenbergh, David
APPLICANT: Persico, Antonio
TITLE OF INVENTION: SEQUENCE OF HUMAN DOPAMINE TRANSPORTER
TITLE OF INVENTION: CDNA
                                                                                                                                                                                                              ADDRESSEE: Birch, Stew
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                    STATE: V
               APPLICATION NUMBER: US/0 FILING DATE: 07-SEP-1994 CLASSIFICATION: 435
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Best Local Similarity
Matches 727; Conserv
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
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LENGTH: 3919 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/REY: misc_RNA
LOCATION: 2724..3117
OTHER INFORMATION: /function= "unknown"
OTHER INFORMATION: /label= VNTR_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
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LOCATION: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
TISSUE TYPE: brainstem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
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                                          CCCATCTGGTACTTGGTGTGTGTCTATTCATCGCATGGCTCATGGTGTTCGGAGTCGTC
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         CCGCGGTGGCAGCTCACAGCCTGCCTGGTGGTCATCGTGCTGCTCTACTTCAGCCTC
                                                                               TACTTTGAACGTGGCGTGCTGCACCTCCACCAGAGCCATGGCATCGACGACCTGGGGCCT
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/product= "HUDAT polypeptide, see Fig. 5 (Hdat)
                                                                                                                                                                                       ----CATCAGTCAACAACATCACCAATGGTACCAGCAGTGCTCAACTC
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Pred. No. 2.1e-40;
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; Sequence 121, Application US/09191468A
; Patent NO. 6416975
; GENERAL INFORMATION:
APPLICANT: Gallagher, Michael J.
APPLICANT: Burgess, Loyd R.
APPLICANT: Brunden, Kurt R.
; TITLE OF INVENTION: Human Glycine Transporter Ty
; FILE REFERENCE: 1231US01
; CURRENT APPLICATION NUMBER: US/09/191,468A
; CURRENT FILING DATE: 1998-11-12
                                                                                                                                RESULT 8
US-09-191-468-121
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; NAME/KEY: CDS
; LOCATION: (1)..(2391)
; OTHER INFORMATION: Seq5
US-09-191-468-121
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Matches 487
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TYPE: DNA
ORGANISM: Human
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PatentIn Ver. 2.0
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                                          ATTTCTGAACTCGCAGGCGTGTTCTGGATTTATGGATTTGGAGAATCTGTGCCTAGACATT
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                                                                                           CAATATATTCTTGAGCTTGTAGATCACTACGGTGGAACATTCCTTGTGCTTTTTCTGCGCC
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                            ATTTTTGAGCTCGTGGGGATCTCTTATGTGTATGGCTTGCAAAGATTCTGTGAAGATATA
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Pred. No. 1.9e-38;
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	Db 330 CTCCTCCTTATACCATCATGGCCATTTTCGGGGGGGATCCCGCTCTTTTACATGGAGCTC 389	QY 368 CTGGTGCCATACGTCATCGTTCTTTACTTGTCGGCAAGCCTGTGTACTACTTAGAGTGT 427		CHRESCOEDO KOOKOONIK KOKOOKOONIK GURUUOOOONIK GURUUOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO	QY 248 GAACGTATGGTATGGTCCAACAACATTGAATTCTTGATGTCCTGCATCGCTACATCCGTC 307	Query Match 6.9%; Score 196.2; DB 1; Length 2278; Best Local Similarity 48.3%; Pred. No. 2.1e-38; Matches 679; Conservative 0; Mismatches 713; Indels 15; Gaps 4;	; NAME/KEY: CDS ; LOCATION: 481868 US-07-959-943-6	IN GENC 2278 b	; TOPOLOGY: Linear ; MOLECULE TYPE: CDNA	; SEQUENCE CHARACTERISTICS: ; LENGTH: 2278 base pairs ; TYPE: nucleic acid	; TELEPHONE: 919-881-3140 ; TELEPAX: 919-881-3175 ; INFORMATION FOR SEQ ID NO: 6:	; REFERENCE/DOCKET NUMBER: 51,000 ; REFERENCE/DOCKET NUMBER: 5405.38a ; TELECOMMUNICATION INFORMATION:	FORMATI Kenneth	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/959,943 FILING DATE: 19921014 CLASSIFICATION: 435	; COMPUTER: EAUPLY UISA ; COMPUTER: IBM PC COMPATIBLE ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.25	; COUNTRY: U.S.A. ; ZIP: 27622 ; COMPUTER READABLE FORM:	NC A		EQUENCES: 12 NCE ADDRESS: : Kenneth D. Sibley; Bell, Selt	Caron, Marc G. NVENTION: Serotonin I	ON: kel	0 10		Ay - 10.7 CUTOCHARANGAGACHUNGTICHTCHTCHTCHTCHTCHTCHTCHTCHTCHTCHTCHTCHTC	1996 GAGATGATTGGATTCCAGCCTAACATCT	
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Best Local S
Matches 679
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TELEFAX: 919-881-31/5
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US/07/959
FILING DATE: 19921014
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1013140
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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CITY: Rale19h
STATE: No. 5418162th Carolina
                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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                                                  GACCTGGGCAACATCTGGCGGTTTCCTTACATATGCTACCAGAATGGCGGAGGGGCCTTC
                                                                     GGTTTGGGTAACGTGTGGCGGTTCCCTTTCATCGCGTACCAGAATGGAGGAGGTGCTTTC
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Pred. No. 2.2e-38;
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   CTGCTCACACTGACGTCAGGAGGGGCATACGTGGTGACTCTGCTGGAGGAGTATGCCACG
                                                                    TGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGGTCATCACGTGCGTCTTGGGATCC
                                                                                                 CCCACCGTCTACATGTCAGCGAT-GACCTGTTCTTGCGGTTTCCTGCTTGGACTTGTTTA
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APPLICANT: Gallagher, Michael J.
APPLICANT: Burgess, Loyd R.
APPLICANT: Brunden, Kurt R.
APPLICANT: Brunden, Kurt R.
TITLE OF INVENTION: Human Glycine Transporter Tyl
FILE REFERENCE: 12311US01
CURRENT APPLICATION UNMBER: US/09/191,468A
CURRENT FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 119
SEQ ID NO 119
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US-09-191-468-119
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; LOCATION: (1)..(2391)
; OTHER INFORMATION: Seq 49
US-09-191-468-119
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Best Local (
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TYPE: DNA
ORGANISM: Human
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                                       CTCGCGTACGAACTCAAGTCAGAGGTGGGAGATGTGGTCGGTGCTGGCGGTACCAGTCTT
                                                                                                  ACTTTGGACACCTTTACAAGTTTCTTGTCTGGGTGCACGATCTTCGGTATCCTTGGTAAC
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     ATGGCCAATGAACGCAAAGTCAACATTGAGAATGTG--
                                                                           TGCACCAACAGTGCCACAAGCATCTTTGCCGGCTTCGTCATCTTCTCCGTTATCGGCTTC
                                                                                                                                                 ACTCTCTCTTACAACAAATTCCACAACAACTGCTACAGGGACACTCTAATTGTCACC
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52.3%;
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Pred. No. 4.7e-38;
0; Mismatches 432;
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                                                                                                                                                                                                    ; OTHER INFORMATION: US-09-191-468-123
                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQ ID NO 123
; LENGTH: 2394
; TYPE: DNA
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APPLICANT: Gallagher, Michael J.
APPLICANT: Burgess, Loyd R.
APPLICANT: Brunden, Kurt R.
APPLICANT: Brunden, Kurt R.
TITLE OF INVENTION: Human Glycine Transporter
FILE REFERENCE: 12311US01
CURRENT APPLICATION NUMBER: US/09/191,468A
CURRENT FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 124
                                                                                                                                Matches
                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2391)
OTHER INFORMATION: SEQ
OTHER INFORMATION: Seq
OTHER INFORMATION: may
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                                                                         GGAGGTCTCGGTGCCCCCATCTGGTACTTGGTGTTGTGTCTATTCATCGCATGGCTCATG
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                                                        GAATATCCTGGCGAGATCAGGTGGCCACTAGCTCTCTGCCTCTTCCTGGCTTGGGTCATT
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                                                                                                                                                                                                                                                      SEQ ID NO:26 [W098/07854 (PCT/US97/14637)] Allelix Sequence; nt 1-2394; nt 304 may be G; nt 371 may be T; nt 836 may, be A; nt 1116 may be G; nt 1831 may be G; nt 2382 may be A or T; nt 2385 may be G;
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52.2%;
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                                                                                                                            Score 193.2; DB 4;
Pred. No. 1.2e-37;
D; Mismatches 433;
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                                                                                                                                                                             Sequence 18, Application US/08700013B Patent No. 5919653
                                                                 GENERAL INFORMATION:

APPLICANT: Albert, Vivian R.

APPLICANT: Kowalski, Leslie R.Z.

APPLICANT: Borden, Laurence A.

APPLICANT: McKelvy, Jeffrey F.

TITLE OF INVENTION: Human Glycine
                                      CORRESPONDENCE ADDRESS:
                                                         NUMBER OF SEQUENCES:
                     ADDRESSEE:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2397 base pairs
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TELEFAX: 609-520-3259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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STRANDEDNESS:
TOPOLOGY: line
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STATE: 1
COUNTRY:
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REFERENCE/DOCKET NUMBER: 31
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CTGTTCTTCCTGATGATGTCGGTGCTGGGTATCGGCTCATCCGTGGCTCTGCTATCGACT
                                                         GCTTTCATTTCATACCCTGATGCCATTGCCAAAACATTCCAACCTCAGCTATTCTCGGTG
                                                                                                                                         CTCGCGTACGAACTCAACTCAGAGGTGGGAGATGTGGTCGGTGCTGGCGGTACCAGTCTT 1225
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                                    ATGTTCTCCTCTTACAACGGTTTCAGACATAATATCTACAGGGATGCTTGGATTGTTACG 1105
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GENERAL INFORMATION:
                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                 FILING DATE:
ATTORNEY/AGENT.INFORMATION:
NAME: BIOOM, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 3177
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kowalski, Leslie R.Z.
APPLICANT: Borden, Laurence A.
APPLICANT: McKelvy, Jeffrey F.
TITLE OF INVENTION: Human Glycine
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Albert, Vivian R.
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                             CLASSIFICATION: 536
RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dechert Price & Rhoads STREET: 997 Lenox Drive, Building CITY: Lawrenceville
                                                                                                                     TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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Pred. No. 1.2e-37;
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RESULT 15 US-09-182-728A-1 ; Sequence 1, Application US/09182728A

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APPLICANT: EVANS, JOANNE RACHEL
APPLICANT: EVANS, JOANNE RACHEL
APPLICANT: CAIRNS, WILLIAM
APPLICANT: HERDON, HUGH
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30176
CURRENT APPLICATION NUMBER: US/09/182,728A
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 9818890.7
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 6
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Best Local Similarity 52.0%;
Matches 484; Conservative
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ACTCTGGGCTGCTTTGTTTCTTCATCATGGGTTTTCCAATGATCACTCAGGGTGGA
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Search completed: July 26, 2003, 03:09:31 Job time : 142 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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US-09-815-923-13

US-09-954-456-560

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US-09-810-107-3339

US-09-817-800A-1429

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            Sequence 4, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 11010, A
Sequence 9, Appli
Sequence 13, Appl
Sequence 560, App
Sequence 560, App
Sequence 377, App
Sequence 377, App
Sequence 3339, Ap
Sequence 1429, Ap
Sequence 1429, Appli
Sequence 3, Appli
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Sequence 5, Appli
Sequence 5, Appli
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Publication No. US20030100479A1
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham
TITLE OF INVENTION: Gene Polymorphisms and Response to Treatment
FILE REFERENCE: D04541
CURRENT APPLICATION NUMBER: US/10/213,948
CURRENT FILING DATE: 2002-08-07
NUMBER OF SEO ID NOS: 40
COURTINE TO THE RESPONSE TO THE PROPERTY OF SEO ID NOS: 40 Query Match 7.2%; Best Local Similarity 48.6%; Matches 727; Conservative SOFTWARE: PatentIn version 3.0 SEQ ID NO 4 LENGTH: 3946
TYPE: DNA
ORGANISM: Homo sapiens 474 419 354 294 239 GAACCGCCAGAACGTATGGTATGGTCCAACAACATTGAATTCTTGATGTCCTGCATCGCT 298 TTAGAGTGTGTCCTCGGACAATTCAGTTCAAGAAACTCTGTTAAAGTTTGGTCAATTTCA 478 CCGGCCATGAAAGGTACTGGATACGCTCAAGCTGCCGGCTGCGGTTACATCCTGTCTTAC 538 ATGGAGCTGGCCCTCGGCCAGTTCAACAGGGAAGGGGCCGCTGGTGTCTGGAAGATCTGC GGTGCTTTCCTGGTGCCATACGTCATCGTTCTTTTACTTGTCGGCAAGCCTGTGTACTAC 418 TTTGCTGTGGACCTGGCCAACGTCTGGCGGTTCCCCTACCTGTGCTACAAAAATGGTGGC ACATCCGTCGGTTTGGGTAACGTGTGGCGGTTCCCTTTCATCGCGTACCAGAATGGAGGA 358 GAGGCCCAGGATCGGGAGACCTTGGGGCAAGAAGATCGACTTTCTCCTGTCCGTCATTGGC 353 GGTGCCTTCCTGGTCCCCTACCTGCTCTTCATGGTCATTGCTGGGATGCCACTTTTCTAC 0; Score 204.8; DB 13; Lung Pred. No. 1e-33; ""amatches 742; Indels Length 3946; 27; Gaps 413 473

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                                                                                     GTAGATCACTACGGTGGAACATTCCTTGTGCTTTTTCTGCGCCCATTTCTGAACTCGCAGGC
                                                                                                                                      GCGACCTTCCTCCTGTCCCTGTTCTGCGTCACCAACGGTGGCATCTACGTCTTCACGCTC
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APPLICANT: Hugh Jonathan Herdon

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GP-30176-D1

CURRENT APPLICATION NUMBER: US/09/795,232

CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 09/182,728

PRIOR FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: 9818890.7

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 2863

TYPE: DNA

ORGANISM: HOMO SAPIENS

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  ATGGCCAATGAACGCAAAGTCAACATTGAGAATGTG---
                                      CTCGCGTACGAACTCAACTCAGAGGTGGGAGATGTGGTCGGTGCTGGCGGTACCAGTCTT 1225
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Israel Simon Gloger
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Indels Length 2863;

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Gaps

1473

1533

1045 1653 1593

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Sequence 3, Application US/09815923

Publication No. US20020197644A1

GENERAL INFORMATION:
APPLICANT: Gill, Sarjeet S.
APPLICANT: The Regents of the University of California FITLE OF INVENTION: Use of Insect Cell Membrane Transporter TITLE OF INVENTION: Target Sites for Insecticides
FILE REFERENCE: 023070-093800US
CURRENT FILING DATE: 2001-03-23

NUMBER OF SEQ ID NOS: 20
SOFTMARE: Patentin Ver. 2.1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            LENGTH: 1764
TYPE: DNA
ORGANISM: Manduca
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Pred. No. 8.6e-31;
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                                                         GGACTTGT--TTACTGCACACCGGGTGGACAATATATTCTTGAGCTTGTAGATCACTACG
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APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, ANI
TITLE OF INVENTION: TOR IDENTIFICATION, ASSESSMENT, PRI
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION UMBER: UG/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
SOFTWARE: FastseQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11010, Application US/10198846 Publication No. US20030099974A1 GENERAL INFORMATION:
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Best Local
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzher
APPLICANT: Steinmann, Ka
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Pred. No. 6.5e-30;
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Sequence 9, Application US/09815923

Publication No. US20020197644A1

GENERAL INFORMATION:
APPLICANT: Gill, Sarjeet S.
APPLICANT: The Regents of the University of California TITLE OF INVENTION: Use of Insect Cell Membrane Transporter TITLE OF INVENTION: Target Sites for Insecticides FILE REFERENCE: 023070-093800US
CURRENT APPLICATION NUMBER: US/99/815,923

CURRENT ETLING DATE: 2001-03-23

NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
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US-09-815-923-9
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US-09-815-923-9
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TYPE: DNA
ORGANISM: Manduca sexta
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                                 ACTTCCTCGCGCTCTTCCCATACGTTGTCATGATCACTTTATTCATCACCACAATCATCC
                                                                 CTTGGGTGTTAGTTTATTTCGCCCTATGGAAAAGCATTAAATCTTCAGCCAAAGTTCGTT
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                                                                                                                                  CTGGTATTGAGT - - - ATCCTGGTGGCATGCGGTGGGAATTGGCAGCTTGCTTGGTCTGTG
                                                                                                                                                            ATGGAATTGAAGGAGGTCTCGGTGCCCCCATCTGGTACTTGGTGTTGTGTCTATTCATCG
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Pred. No. 1.5e-27;
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                                                                     GAAGACTGTCTAGAAATATTAAACAAATGACAGGTCGCCAACCATCGCTATACTTTCGAT
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APPLICANT: Gill, Sarjeet S.
APPLICANT: Ross, Linda S.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A
TITLE OF INVENTION: Target Sites for Insecticides
TILE REFERENCE: 023070-093800US
CURRENT APPLICATION NUMBER: US/09/815,923
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 3513
TYPE: DNA
ORGANISM: Manduca sexta
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US-09-815-923-13

Sequence 13, Application US/09815923 Publication No. US20020197644A1 GENERAL INFORMATION:

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; OTHER INFORMATION: GABA transporter
US-09-815-923-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
                                                                                                                                               PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: US/
                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/60/235,720 PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION NUMBER: US/60/234,923
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PRIOR APPLICATION NUMBER: US/60/234,052
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                                                                                                        NUMBER OF SEQ ID NOS: 2276
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PRIOR FILING DATE: 2000-09-27
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1630
LENGTH: 2283
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Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
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PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
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US-09-954-456-1630
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ORGANISM: Homo sapiens
FEATURE:
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TCTGGGTGCACGATCTTCGGTATCCTTGGTAACCTCGCGTACGAACTCAACTCAGAGGTG 1192
                                               AACAACTGCTACAAGGATGCCATCATCCTGGCACTCATCAACAGCGGGACCAGCTTCTTT
                                                                            CATAATATCTACAGGGATGCTTGGATTGTTACGACTTTGGACACCTTTACAAGTTTCTTG
                                                                                                                                                  TTCTCTCTGACAGTGTGCACCGGACCGATCATCATGTTCTCCTCTTACAACGGTTTCAGA 1072
                                                                                                                                                                                                                    CCTCAATGGGCGAAACTCCTTGAGCTCGGTGTATGGTACTCAGCAGTCACGCAAGTGTTC
                                                                                                                                                                                                                                                       CTGCTGGTGCGTGCTGCTGCCTGGCGCCCCTGGATGGCATCATTTACTATCTCAAG
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                                                                                                                   TTCTCTTATGCCATCGGCCTGGGGGCCCTCACAGCCCTGGGCAGCTACAATCGCTTCAAC
                                                                                                                                                                                     CCTGACTGGTCAAAGCTGGGGTCCCCTCAGGTGTGGATAGATGCGGGGACCCAGATTTTC
                                                                                                                                                                                                                                                                                                                        AAATCCACGGGAAAGATCGTGTACTTCACTGCTACATTCCCCTACGTGGTCCTGGTCGTG
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pred. No. 2.4e-24;
0; Mismatches 789;
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RESULT 9
US-09-19-039-377
Sequence 377, Application US/09919039
Publication No. US20030108871A1
GENERAL INFORMATION:
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                                                                                                                                   GTGTTCTTCTACGCTCTTCTCGCCTCTAACAACCTGGTGTTTCGGAGACAACTACGTATAC 1714
                                                                                                                                                                                                                                                                                CGACCTTGCCCCTGGATGAAATGGTGCTGGTCCTTCTTCACCCCGCTGGTCTGCATGGGC 1617
                                                                                                                                                                                                                                                                                                                                                                             GTGTTCTGGATTTATGGATTGGAGAATCTGTGCCTAGACATTGAGTTCATGTTGGGTAAA 1594
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                                                                                                                                                                   CCGACTGCTGGTTATGTTTCTGGATACTTGATGTTATTTTTTGGGCATGACGTTTGTGCC
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PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 377
LENGTH: 2919
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                      OTHER INFORMATION: Incyte ID No. US-09-919-039-377
Query Match
Best Local Similarity
Matches 738; Conserv
                                                                                                                                                                                                                                                                                                                          APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0.035 US

CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09
                                                                                                                          NAME/KEY: misc_feature
        Conservative
                        5.48;
      0;
    Score 154.8; DB 12;
Pred. No. 4.9e-23;
0; Mismatches 812;
                                                                                                         US20030108871A1 5834958CB1
        Indels
                                           Length 2919
        36;
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221 GACACGGACTTAGAGGCTGAACCGCCAGAACGTATGGTATGGTCCAACAACATTGAATTC 280 GACCAGGAAGACGAGGACCAGGTGAAGGATCGGGGCCAATGGACCAACAAGATGGAGTTT

401 316 461 376 341 256

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TTGATGTCCTGCATCGCTACATCCGTCGGTTTGGGTAACGTGTGGCCGGTTCCCCTTTCATC
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                                                  TICTICCTGATGATGTCGGTGCTGGGTATCGGCTCATCCGTGGCTCTGCTATCGACTTTC
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                                                                                                                                         TTCATTCATACCCTGATGCCATTGCCAAAACATTCCAACCTCAGCTATTCTCGGTGCTG
                                                                                                                                                                                                                        GCGTACGAACTCAACTCAGAGGTGGGAGATGTGGTCGGTGCTGGCGGTACCAGTCTTGCT 1228
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                         TTCTTTATCATGCTCATATTCCTAGGGCTGGACAGCCAGTTTGTCTGTGTGGAGTGCCTG
                                                                                                     ATGTCCCAAGAGCAAGGGGTGCCCATTTCTGAAGTGGCCGAGTCAGGTCCTGGGCTGGCC
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US-09-880-107-3339
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SEQ ID NO 3339
LENGTH: 3410
TYPE: DNA
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APPLICANT: Gene Logic, Inc.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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APPLICANT: Vockley, Josep
APPLICANT: Scherf, Uwe
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                                                                                                                                              TYPE: DNA
 Local Similarity hes 699; Conserv
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Sequence 1429, Application Patent No. US20020119462A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,029
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TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
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APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/297,457 PRIOR FILING DATE: 2001-06-13
                                                                                                                              ORGANISM: Rattus norvegicus FEATURE: OTHER INFORMATION: Genbank
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FILLING DATE: 2001-05-11
APPLICATION NUMBER: US 60/290,645
FILLING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/292,336
FILING DATE: 2001-05-22
APPLICATION NUMBER: US 60/295,798
FILING DATE: 2001-06-06
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Castle, Arthur
Elashoff, Michael
     Conservative
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Score 147.6; DB 1
Pred. No. 1.4e-21;
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                                ACATTCCAACCTCAGCTATTCTCGGTGCTGCTGTTCTTCCTGATGATGTCGGTGCTGGGTATC 1318
                                                                                                                                                                                                                      TGCTACAGGGACTGCGTCGCCCTTTGCATTCTCAACAGCAGCACCAGCTTCGTGGCCGGG
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                                                                                                           GTGGTCGGTGCTGCGGTACCAGTCTTGCTTTCATTCATACCCTGATGCCATTGCCAAA
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TGGATACGCTCAAGCTGCCGGCTGCGGTTACATCCTGTCTTACTACGTGGTGATCTGTGG
                                                                                                         TTTCATTATGTTAATGATCGGAGGACTTCCCATGTTCTATATGGAACTTGTACTCGGACA
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                                                               TTCTACGCTCTTCTCGCCTCTAACAACCTGGTGTTCGGAGACAACTACGTATACCC 1716
                                                                                                                              TGGCCTCTTATCAAATACTGTTGGCTCTTTTTCACGCCAGCTGTGTGCCTGGCAACCTTC 1649
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Sequence 1, Application US/09843598
Patent No. US20020010944A1
GENERAL INFORMATION:
APPLICANT: HOTVITZ, H. Robert
APPLICANT: Ranganathan, Rajesh
                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/843,598
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200,549
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2016
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ranganathan, Rajesh
TITLE OF INVENTION: CeSERT GENES,
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: 01997/525002
                                                                                                         Similarity
                      ATGGTCCAACACTTGAATTCTTGATGTCCTGCATCGCTACATCCGTCGGTTTTGGGTAA 318
                                                                                                                                                                                                Caenorhabditis
ATGGGCAACTAAAATGGAATTCCTGTTGGCCGTCGTTGGATATGCAGTTGATTTGGGTAA
                                                                                       Conservative
                                                                                                       5.18;
                                                                                                                                                                                           elegans
                                                                                       0;
                                                                                  Score 146.8; DB 10;
Pred. No. 2.1e-21;
0; Mismatches 722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEINS,
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    TGATCAGTTCTCAAAAGATATTCGTGCTATGCTGGGATTCTATCCTGGAATTTATTGGAG
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; Patent No. US20020010944A1
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Ranganathan, Rajesh
; TITLE OF INVENTION: COSERT GENES, PROTITLE OF INVENTION: COMPOUNDS
; FILE REFERENCE: 01997/525002
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CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200,549
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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  CGGCAAAGCGGCCTACTTCCTCGCGCTCTTCCCCATACGTTGTCATGATCACTTTATTCAT
                                                                     GTGTCTATTCATCGCATGGCTCATGGTGTTCGGAGTCGTCGCCCGAGGAGTCAAGAGTTC
                                                                                                                                TGAAGTTCAAAAATCAACAGGATTCGATGATCTTGGAGGTGTAAAAACTTCAATGGCAGT
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Pred. No. 2.1e-21;
0; Mismatches 722;
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APPLICANT: Ranganathan, Rajesh
TITLE OF INVENTION: CESERT GENES, PROTEINS, AN
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: 01997/525002
CURRENT APPLICATION NUMBER: US/09/843,598
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200,549
PRIOR FILING DATE: 2000-04-26
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-843-598-2
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APPLICANT: Horvitz, H. Robert
APPLICANT: Ranganathan, Raje
                                                                                                                                                                                                                   Sequence 2, Application US/09843598 Patent No. US20020010944A1
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; ORGANISM: Caenorhabditis elegans
US-09-843-598-2
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Best Local S
Matches 484
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APPLICANT: Ross, Linda S.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Use of Insect Cell Membrane Transporters
TITLE OF INVENTION: Target Sites for Insecticides
FILE REFERENCE: 023070-093800US
CURRENT APPLICATION NUMBER: US/09/815,923
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09815923 Publication No. US20020197644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1671
TYPE: DNA
ORGANISM: Manduca sexta
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                     259 ATGGTCCAACAACATTGAATTCTTGATGTCCTGCATCGCTACATCCGTTCGGTTAGGGTAA 318
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                                                                         CGTCATCGTTCTTTTACTTGTCGGCAAGCCTGTGTACTACTTAGAGTGTGTCCTCGGACA 438
                                                                                                                CCTATGGCGGTTTCCCTATTTGTGTTATCGGAATGGAGGAGGAGCGTTTTTGATTCCGTA 143
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                                                                    TGGGTTAGCATTTGTTACGTACCCGGCTACGGTGACGATGATGCCAGCTCCTAATTTGTG
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Search completed: July 26, 2003, 05:39:32 Job time : 622 secs

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 62-63; 71pp; English.
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                                 GLENICLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGY
                                                                       FKGWKYWKVALTTSVCGFLMGLVYVTPGGQWILTLVDFYGGTYVVFILAIFELAGIVWVY
                                                                                             FPRVPTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGVFWIY
                                                                                                                                                VV-RSGTGLAFISYPDAISK-FQAVPQLFSVLFFFMLFVLGIGSIVALQSTIVTIICDQ
                                                                                                                                                                        DVVGAGGTSLAFISYPDAIAKTFQ--PQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMDA
                                                                                                                                                                                                                           LTVCTGPIIMESSYNGERHNIYRDAWIVTTLDTETSELSGCTIEGILGNLAYELNSE-VG
                                                                                                                                                                                                                                                                                                   SGKAAYFLALFPYVVLFVLLIRAVTLEGARDGILFFLEPQWGELLNPTVWKEAVVQCFFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLALTLYYLFVSFQSELPWSYCRDEWTNCVNSRP--QEYVDNLLTGVSLANESARNLSGI 194
                                                                                                                                                                                                                                                                                                                                                                                                    -----SSAQLYFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGVVARQVKS
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Pred. No. 4e-156;
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                                                                                                                                                                                                                                                                                                                                                                                        useful in developmental biology and in elucidating cell signalling and inelucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG511), expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form specification, but was obtained in electronic 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid
genes from Drosophila and
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11-JUL-2000;
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                                           VWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEWENCVPS
                                                                                                                  MSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVK
                                                                                       MSCISVSVGLGNVWRFPFTAYENGGGAFLIPYIIVLFLIGKPMYYLEMIMGQFTSQGTVK
IWSVVPGFVGVGYGQAFGTICIISYYSSLLALTLYYLFVSFQSELPWSYCRDEWTNCVNS
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                                                                                                                                                                                    Score 1523; DB 22;
Pred. No. 1.9e-150;
7; Mismatches 170;
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format directly from
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                          New isolated nucleic a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBD57737-ABB72072).
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RYQLFVQEGNANALFRRSS-----IWHKI
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                                                                                                             GYLMLFLGMTFVPIGIGFSLY------KYRTGTFSETIKKAFHSKPSWGPRSPRERR
                                                                                                                                                  KRLCRDVEFMIGIKTSLYYRICWAVVTPLLMLTILIYTLVLYEPLKYKD-YTYQSGVYVF
                                                                                                                                                                   ENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVS
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ABB71178 standard; Protein; 639 A

ABB71178;

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Drosophila melanogaster polypeptide SEQ ID NO 40326

Drosophila; developmental biology; cell signalling;

pharmaceutical

Drosophila melanogaster

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[ABB57737-ABB72072].
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RDREPNEGOWQCSLLIAVVSEFIGLMYITPGGQYMLTLVDEFGASMIALVLGIAELYTIG
             MDAFPRVPTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGVF
                                                 DIGSVV-KGGAGLAFISYPDAIAK-FKNLPQIFSVLFFLMLFVLGIGSNIAMTSCSVTAI
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          cc candidate compound especially a putative pesticidal or pharmaceutical cagent that interacts with an invertebrate symporter cell surface cc receptor protein or its fragment. Insect or worm genetically modified to express protein of the invention is useful for studying invertebrate symporter cell surface receptor protein activity, by detecting the phenotype caused by the expression or mis-expression of the protein in the animal. Nucleic acids encoding the invertebrate receptor protein or their fragments are useful as biopesticides. SNF nucleic acids are useful for generating mutant phenotypes in an animal model or living cells that are useful as pesticide or drug targets. The genetically modified organisms or cells are useful in screening assays to identify pesticides or therapeutics and thus are useful in the identification of new drug targets, therapeutic agents, diagnostics and prognostics. The useful in treatment of disorders associated with ion channels. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000;
23-MAR-2000;
23-MAR-2000;
                                                                                                                                                                                                                                                            The invention relates to invertebrate symporter cell surface recomposition of the sodium/neurotransmitter family (SNF) and nucleic acid mole encoding such receptors. The SNF protein is useful for detecting
                                                                                                                                                                                                                                                                                                                                                             Novel invertebrate symporter cell surface receptor proteins and nucleic acid encoding the protein useful as pesticide or drug target and to identify compounds that have utility as therapeutics or pesticides
                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 67-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kellerman KA,
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15-MAR-2000;
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2000US-0189399.
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                                                                                      Drosophila melanogaster polypeptide SEQ
                                                                                                                                           ABB64027 standard;
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                                           Drosophila melanogaster
                                                            Drosophila; dev pharmaceutical.
                                                                                                        26-MAR-2002
                                                                                                                           ABB64027;
                           WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                     IAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVKVWSISPAMKGTGYAQAAG
                                                                                                                                                                                                                                                                    WIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPT
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                                                                                                                                                                                                                                                                                                                                          EVGDVVGAGGTSLAFISYPDAIAKTFQ--PQLFSVLFFLMMSVLGIGSSVALLSTFNTLA 420
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                                                                                                                                                                                                       FKAEAKALRQKMNTSRVKHLWYSITGAYRRNI 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639 AA;
                                                                     developmental biology;
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                                                                                                                                                                                      HKEIENELTPKRGQGIW----AAIKQNI
                                                                                                                                            Protein;
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Pred. No. 4.2e-145;
7; Mismatches 200;
                                                                                                                                            B
                                                                     cell signalling; insecticide;
                                                                                      ID NO 18873
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                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 18873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000;
                                                                             Sequence
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)B; ABL08130.
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                                                                             629 AA;
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2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
Score 1414; DB 22;
Pred. No. 5.6e-139;
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                       Length 629
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Matches Local Similarity 182 481 473 421 361 354 301 294 241 176 122 62 56 10 GVWYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGIL NNIEFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFS FESSEPKMEPKRSSQISLPPANNKAALDNIDDTDLEAEPPE-------GNLAYELNSEVGDVVGAGGTSLAFISYPDAIAK-TFQPQLFSVLFFLMMSVLGIGSSVAL 412 VIIGTILSKGIRSSGKASYFLALFPYVIMIVLLIRAVTLPGAWQGIVYFLKPQWSQLLNP LMVFGVVARGVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLEL SRGCIRAFDMAPIMRGIAYGQVYSTALATTYYACIMALTIRYLVASFSEVLPWTYCLVEW YQKLRRNMQGAQGSREGHPGSN-----DGISTVIYSAEGEELTINCEAESESSGQRDQWS GDNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPSWGPRSP IAELVAVGWIYGVKRICSDIEFMLNVKTSFYWRICWAIVAPGLMFLVLVYMLFSYEPLTY ISELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVF GNLAFETNTKDISQVVKGGAGLAFISYPEAIAKFKYLPQLFAVLFFFMLLVLGIGSNIGM HVWYAAITQMFFSLAICFGTLVMYASFNDFNKNVHKDVIIITTIDSLTSILAGCIIFGIL GKSCVATGAT-AANDSSIVQGVSSAELFFTQTVLREPESLDDNGLGTPSWDLVLCLLATW -ENCVPSDPTLAASVNNITNGTSSAQLYFLRTVLQQSDGI-EGGLGAPIWYLVLCLFIAW SRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEW Conservative 113; Mismatches Indels 36; -RMVWS Gaps 115 181 61 532 480 472 420 360 353 300 293 240 233 175 121 55 9

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  Drosophila melanogaster Bioamine Transporter 1 (BT1) nucleic acid and protein, useful in screening assays to identify candidate compounds which are potential pesticide agents or therapeutics that interact with BT1 proteins -
                                                                                                                                                                                                                                            09-SEP-1999;
                                                                                                                                                                                                                                                                                  08-SEP-2000;
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Domain
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DB; AAD03450.
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137..157
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/note= "Sodium neurotransmitter symporter
specifically claimed in claim 1"
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Best Local Similarity 43.9
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                  ABB60692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragments, such as an antisense sequence or double stranded RNA, may be used as a biopesticide to inhibit BTI function. The invertebrate model organisms such as Drosophila melanogaster are useful for rapidly carrying out large-scale systematic genetic screens and therefore for analysing expression and mis-expression of BTI protein.
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                                                                                                                                                                                                                                                                           IAELLAVGWIYGVKRICSDIEFMLNVKTSFYWRICWAIVAPGLMFLVLVYMLFSYEPLTY
                                                                                                                                                                                            -RGVQYPPVYYMAGWIIWGLGVLQLPFWALVTIYQQPGKTFGSKFGLAMQPTANWGPLQT
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                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                            Sequence
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11-JUL-2000;
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                               AMSFQATLPWAICQPEW-ENCVPSDPTLAASVNNITNGTSSAQLYFLRTVLQQSDGIEGG
                                                                                                                 FDSFASELPWSFCREEWGDGCVSASGGQPLQGQLSRNFSSSTQLYLQRIVLNETDSLEEG
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The invention relates to invertebrate symporter cell surface receptors of the sodium/neurotransmitter family (SNF) and nucleic acid molecules encoding such receptors. The SNF protein is useful for detecting a candidate compound especially a putative pesticidal or pharmaceutical agent that interacts with an invertebrate symporter cell surface receptor protein or its fragment. Insect or worm genetically modified to express protein of the invention is useful for studying invertebrate symporter cell surface receptor protein activity, by detecting the phenotype caused by the expression or mis-expression of the protein in the animal. Nucleic acids encoding the invertebrate receptor protein or their fragments are useful as biopesticides. SNF nucleic acids are useful for generating mutant phenotypes in an animal model or living cells that are used to study the regulation of genes encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1999;
15-MAR-2000;
23-MAR-2000;
23-MAR-2000;
                                                                                                                                                                                                                                         Novel invertebrate symporter cell surface receptor proteins and nucleic acid encoding the protein useful as pesticide or drug target and to identify compounds that have utility as therapeutics or pesticides -
                                                                                                                                                                                                                    Claim 18;
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strychnine-sensitive glycine receptor; treatment; diagnosis; nervous system disorder; myocionus; muscle spasm; hyperactivity; epilepsy; spasticity; head trauma; neuronal cell death; multiple sclerosis; spinal cord injury; Huntington's disease; amyotrophic lateral sclerosis.
                                                                                                                                       Human; GlyT-2 transporter; glycine transporter;
activity; N-methyl-D-aspartate receptor; NMDA;
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                                                                                                           VYLVILLIRGVTLPGAGAGIWYFITPKWEKLTDATVWKDAATQIFFSLSAAWGGLITLSS
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RESULT 12
AAW56369
ID AAW56
                                                                                                                                           Human; GlyT-2 transporter; glycine transporter; neurotransmi activity; N-methyl-D-aspartate receptor; NMDA; strychnine-sensitive glycine receptor; treatment; diagnosis;
                                                                                           nervous system
epilepsy; spast
multiple sclerc
                                                                                                                                                                                                                                                                                                                                            AAW56369
WO9807854-A1
                                                                       amyotrophic lateral
                                                                                                                                                                                                                        Amino acid sequence of a human GlyT-2 transporter protein
                                                                                                                                                                                                                                                                    29-JUL-1998
                                                                                                                                                                                                                                                                                                        AAW56369;
                                     HOMO
                                   sapiens
                                                                                           scierosis;
                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                           ystem disorder; myoclonus; muscle spasm; hype spasticity; head trauma; neuronal cell deatl
                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                         sclerosis
                                                                                         spinal cord injury;
                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                            797
                                                                                                                                                                                                                                                                                                                                            AA
                                                                                           Huntington's
                                                                                                                                                                                     neurotransmitter;
                                                                                                                               hyperactivity;
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26-FEB-1998

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IMFVIKMH-LAPGRFIERLKLVCSPQPDWGPFLAQHRGE

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a variant of the human GlyT-2 transporter. The cDNA encoding GlyT-2 was generated by reverse transcription PCR (RT-PCR) from human spinal cord or cerebellum polyA mRNA. GlyT-2 is a glycine transporter found predominantly in the brain stem and the spinal cord. GlyT-2 regulates the levels of glycine, a major neurotransmitter, that preferentially influences the activity of N-methyl-D-aspartate (NNDA) receptors and strychnine-sensitive glycine receptors. The GlyT-2 protein can be used to treat or to diagnose a nervous system disorder or condition, e.g. pain, myoclonus, muscle spasm or hyperactivity, epilepsy or spasficity associated with stroke, head trauma, neuronal cell death, multiple sclerosis, spinal cord injury,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders, e.g. pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human glycine transporter -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Albert VR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ALLX )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-1996;
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559
                                                                499
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B; AAV22906.
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                                                                                                                                                                                   DAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMDAFPRVPTVYMSAMT---CS
                                                                                                                                                        EALTRLPLSPFWAIIFFLMLLTLGLDTMFATIETIVTSISDEFPKYLRTHKPVFTLGCCV
                                                                                                                                                                                                                                                  GFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNSEVGDVVGAGGTSLAFISYP
                                                                                                                                                                                                                                                                                                                                                            YFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGVVARGVKSSGKAAYFLALFPYVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WSSKLDFILSMVGYAVGLGNVWRFPYLAFQNGGGAFLIPYLMMLALAGLPIFFLEVSLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WSNNIEFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQ 113
                                 QPNIFWKVCWAFVTPTILTFILCFSFYQWEPMTYG-SYRYPNWSMVLGWLMLACSVIWIP
                                                              KTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVSGYLMLFLGMTFVP
                                                                                              CFFIMGFPMITQGGIYMFQLVDTYAASYALVIIAIFELVGISYVYGLQRFCEDIEMMIGF
                                                                                                                         CGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGVFWIYGLENLCLDIEFMLGK 498
                                                                                                                                                                                                                     KFHNNCYRDTLIVTCTNSATSIFAGFVIFSVIGFMANERKVNIENVADQ-GPGIAFVVYP
                                                                                                                                                                                                                                                                                LVILLIRGVTLPGAGAGIWYFITPKWEKLTDATVWKDAATQIFFSLSAAWGGLITLSSYN
                                                                                                                                                                                                                                                                                                           MITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSAVTQVFFSLTVCTGPIIMFSSYN
                                                                                                                                                                                                                                                                                                                                                                                                       PWNTPECKDKTKLLLDSCVISDHPKIQIKNSTFCMTAYPNVTMVNFTSQANKTFVSGSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FASQGPVSVWKAIPALQGCGIAMLINSVLIAIYYNVIICYTLFYLFASFVSVLPWGSCNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQP
 IGIGFSLYKYRTGTFSETIKKAFHSKPSWGPRSPRERRE
                                                                                                                                                                                                                                                                                                                                            YFKYFVLKISAGIEYP-GEIRWPLALCLFLAWVIVYASLAKGIKTSGKVVYFTATFPYVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huntington's disease or amyotrophic lateral sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pages
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US14637
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38.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ENCVPSD-PTL-----AASVNNIT--NGTSSA-----QL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kowalski LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1084.5;
Pred. No. 3e-1
06; Mismatches
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RESULT 13
AAY82115
ID AAY82212
XX AAY822
XX O5-JU
XX Human
XX Human
XX Human
XX Human
XX Homo
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents the human SC polypeptide glycine transporter. The polypeptide is useful in a method for screening identify compounds which stimulate or inhibit the function of the polypeptide and in a process for diagnosing a disease or a susceptibility to a disease in a subject related to expression or activity of the polypeptide e.g. treatment of neuropathic pain, or pain, spasticity, myoclonus, epilepsy, stroke, head trauma, spinal injury, dystonia, multiple sclerosis, armyotrophic lateral sclerosis, and the polypeptide e.g. treatment of neuropathic pain, or pain, spasticity, myoclonus, epilepsy, stroke, head trauma, spinal injury, dystonia, multiple sclerosis, armyotrophic lateral sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identification; neuropathic pain; spasticity; myoclonus; epistroke; head trauma; spinal cord injury; dystonia; multiple arnyotrophic lateral sclerosis; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY82115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huntington's disease or Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 17-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polypeptides and polynucleotides, useful for screening for (ant)agonists and for diagnosing a disease e.g. spasticity, epilepsy, stroke, multiple sclerosis, Huntington's disease or Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
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identification; neuropathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-258613/23.
DB; AAZ95536.
                                                                                                                                                                 174
374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                 EW--
                                                                                                                                                                                                                                                                                                                                                            WSNNIEFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein;
                                                     YFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGVVARGVKSSGKAAYFLALFPYVV 261
                                                                                                                                                                                                                    FASQGPVSVWKAIPALQGCGIAMLIISVLIAIYYNVIICYTLFYLFASFVSVLPWGSCNN
                                                                                                                                                                                                                                                                       FSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQP 173
                                                                                                                                                                                                                                                                                                                             {\tt WSSKLDFILSMVGYAVGLGNVWRFPYLAFQNGGGAFLIPYLMMLALAGLPIFFLEVSLGQ}
YFKYFVLKISAGIEYP-GEIRWPLALCLFLAWVIVYASLAKGIKTSGKVVYFTATFPYVV
                                                                                                        PWNTPECKDKTKLLLDSCVISDHPKIQIKNSTFCMTAYPNVTMVNFTSQANKTFVSGSEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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                                                                                                                                                              ENCVPSD-PTL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                      105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1082.5; DB 2
Pred. No. 4.9e-104;
5; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transporter
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                                                                                                                                                              ---AASVNNIT--NGTSSA-----
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RESULT 14
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                 The present sequence is a mutant version of the protein sequer human glycine transporter type 2 (GlyT2). Glycine is involved neurotransmission in the spinal cord and cerebellum, where gly
                                                                                           Claim 4;
                                                                                                                                                                                                                                              Gallagher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human glycine transporter type;
epilepsy; stroke; head trauma; r
dystonia; Huntington's disease;
                                                                                                                                          whether an animal has
                                                                                                                                                                                                                                                                                                                 12-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                                                                              , PW
                                                                                                                                    acid encoding a human glycine transporter type 2 (Gl
expressing GlyT2 which can then be used for detecting
animal has autoimmune antibodies against a glycine
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   where glycine
GlyT2 gene and
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epilepsy;
multiple;
                                                                                                                    Amino
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 ; spasticity; head
sclerosis; spinal
                                                                                                                    sequence
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protein could, therefore, we used to identify inhibitory compounds which prevent GlyT2 activity, causing a decrease in muscle hyperactivity. They could be used to treat diseases or conditions associated with muscle contraction, including muscle spasticity (such as that due to epilepsy, stroke, head trauma, multiple sclerosis, neuronal cell death, spinal cord injury and dystonia), myoclonus, epilepsy, Huntington's disease, amyotrophic lateral sclerosis and pain.

Note: This sequence is not shown in the specification, but is derived from the hGlyT2 wild type sequence shown in SEQ ID NO: 124 (AAB09898).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                             MT---CSCGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGVFWIYGLENLCLD
CSVIWIPIMFVIKMH-LAPGRFIERLKLVCSPQPDWGPFLAQHRGE
                                                 LGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPSWGPRSPRERRE
                                                                                                      IEMMIGFQPNIFWKVCWAFVTPTILTFILCFSFYQWEPMTYG-SYRYPNWSMVLGWLMLA
                                                                                                                                                        IEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVSGYLMLF
                                                                                                                                                                                                            FTLGCCICFFINGFPMITQGGIYMFQLVDTYAASYALVIIAIFELVGISYVYGLQRFCED
                                                                                                                                                                                                                                                                                                                     IAFVVYPEALTRLPLSPFWAIIFFLMLLTLGLDTMFATIETIVTSISDEFPKYLRTHKPV
                                                                                                                                                                                                                                                                                                                                                                    LAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMDAFPRVPTVYMSA
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Pred. No. 6.2e-104;
6; Mismatches 218;
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768
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AAW56372 standard;
(first
                                 Protein;
entry)
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Human; GlyT-2 transporter; glycine transporter; neurotransmi activity; N-methyl-D-aspartate receptor; NMDA; strychnine-sensitive glycine receptor; treatment; diagnosis; nervous system disorder; myoclonus; muscle spasm; epilepsy; spasticity; head trauma; neuronal cell o of a human GlyT-2 transporter neurotransmitter; hyperactivity; protein

spinal

cord

injury;

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human GlyT-2 transporter protein. The cDNA encoding GlyT-2 was generated by reverse transcription PCR (RT-PCR) from human spinal cord or cerebellum polyA mRNA. GlyT-2 is a glycine transporter found predominantly in the brain stem and the spinal cord. GlyT-2 regulates the levels of glycine, a major neurotransmitter, that preferentially influences the activity of N-methyl-D-aspartate (NMDA) receptors and strychnine-sensitive glycine receptors. The GlyT-2 protein can be used to treat or to diagnose a nervous system disorder or condition, e.g. pain, myoclonus, muscle spasm or hyperactivity, epilepsy or spasticity associated with stroke, head troums, neuronal cell death, multiple solerosis, spinal cord injury, associated with stroke and troums, neuronal cell death, multiple solerosis, spinal cord injury, associated with stroke and sections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amyotrophic lateral sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Pages 55-56; 90pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human glycine transporter - useful for treating nervous system disorders, e.g. pain, myoclonus, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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DB; AAV22909.
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439 CGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGVFWIYGLENLCLDIEFMLGK 498
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                                                                                                                                                                                                                                 262 MITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSAVTQVFFSLTVCTGPIIMFSSYN 321
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                                                                                                                                                             GFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNSEVGDVVGAGGTSLAFISYP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSSKLDFILSMVGYAVGLGNVWRFPYLAFQNGGGAFLIPYLMMLALAGLPIFFLEVSLGQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSNNIEFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQ 113
                                                                                      DAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMDAFPRVPTVYMSAMT---CS
                                                                                                                                                                                                LVILLIRGVTLPGAGAGIWYFITPKWEKLTDATVWKDAATQIFFSLSAAWGGLITLSSYN
                                                                                                                                                                                                                                                                                                                                                                                                                 FASQGPVSVWKAIPALQGCGIAMLIISVLIAIYYNVIICYTLFYLFASFVSVLPWGSCNN 313
                                                       EALTRLPLSPFWAIIFFLMLLTLGLDTMFATIETIVTSISDEFPKYLRTHKPVFTLGCCI
                                                                                                                          KFHNNCYRDTLIVTCTNSATSIFAGFVIFSVIGFMANERKVNIENVADQ-GPGIAFVVYP
                                                                                                                                                                                                                                                                      YFKYFVLKISAGIEYP-GEIRWPLALCLFLAWVIVYASLAKGIKTSGKVVYFTATFPYVV
                                                                                                                                                                                                                                                                                                       YFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGVVARGVKSSGKAAYFLALFPYVV 261
                                                                                                                                                                                                                                                                                                                                            PWNTPECKDKTKLLLDSCVISDHPKIQIKNSTFCMTAYPNVTMVNFTSQANKTFVSGSEE
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Pred. No. 7.9e-104;
06; Mismatches 213;
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731 IMFVIKMH-LAPGRFIERLKLVCSPQPDWGPFLAQHRGE 768	731 IME	ф	
559 IGIGFSLYKYRTGTFSETIKKAFHSKPSWGPRSPRERRE 597	559 IGIO	Qy	
672 QPNIFWKVCWAFVTPTILTEILCESEYQWEPMTYG-SYRYPNWSMVLGWLMLACSVIWIP 730	672 QPN	Db	
499 KTGAYWRLCWGVITPAIMTTVFEYALLASNNLVFGDNYVYPTAGYVSGYLMLFLGMTFVP 558	499 KTG2	Qу	
612 CFFIMGFPMITQGGIYMFQLVDTYAASYALVIIAIFELVGISYVYGLQRFCEDIEMMIGF 671	612 CFF:	Db	

Search completed: July 21, 2003, 09:29:29 Job time: 74 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
2: pir2:*
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A46270
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B44409
A44409
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gamma-aminobutyri
glycine transport
                            taurine transport GABA/beta-alanine
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gamma-aminobutyri
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                                                                                                                                                                                                                                                                                                           Description
        dopamine
                taurine transport
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       transpor
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A;Molecule type: mRNA A;Residues: 1-799 <LIU> A;Cross-references: GB:L21672 C;Genetics:

Gene: GLYT2

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
820	861	867.5	902	920.5	929	929.5	929.5	932.5	933	934.5	935	935	935	936	940.5
24.4	25.7	25.9	26.9	27.4	27.7	27.7	27.7	27.8	27.8	27.9	27.9	27.9	. 27.9	27.9	28.0
632	615	579	693	617	602	597	590	614	619	619	638	633	633	615	614
2	N	N	N	N	N	N	N	N	N	2	Ν	N	N	N	2
T24405	T43330	D88551	A41617	S14278	I55651	S65673	A47194	S68236	I59558	S20346	JH0673	S23151	I58140	S43285	A41757
hypothetical prote	catecholamine tran	protein T23G5.5 [i	dopamine transport	noradrenaline tran	noradrenaline tran	GABA transport pro	taurine and beta-a	betaine/GABA trans	dopamine transport	dopamine transport	glycine transport	glycine transporte	glycine transporte	noradrenaline tran	betaine transport

ALIGNMENTS

RESULT 1 A48716

glycine transporter GLYT2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Pattus norvegicus (Norway rat)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 02-Jun-1995
C;Accession: A48716
R;Liu, Q.R.; Lopez-Corcuera, B.; Mandiyan, S.; Nelson, H.; Nelson, N.
J. Biol. Chem. 268, 22802-22808, 1993
A;Title: Cloning and expression of a spinal cord- and brain-specific glycine transpor A;Reference number: A48716
A;Reference number: A48716
A;Accession: A48716
A;Status: preliminary
A;Corcurate Control of the co

Qy	ΔQ	Oy	Db	Qy	Db	Qy	Db	Qγ	Db	Qy	Db	Qy	Db	Qy	Query Best Matcl	1
423 AFPRVPTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGV 479			476 IFFSLSAAWGGLITLSSYNKFHNNCYRDTLIVTCTNSATSIFAGFVIFSVIGFMANERKV 535	303 VFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNS 362	416 GIKTSGKVVYFTATFPYVVLVILLIRGVTLPGAGAGIWYFITPKWEKLTDATVWKDAATQ 475	243 GVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSAVTQ 302	357 TMVNFTSQANKTFVSGSEEYFKYFVLKISAGIEYP-GEIRWPLPFCLFLAWVIVYASLAK 415	193 TNGTSSAQLYFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAMLMVFGVVAR 242	297 LEYLFASEVSVLPWGSCNNPWNTPECKDKTKLLLDSCVIGDHPKIQIKNSTFCMTAYPNL 356	155 LYYLAMSFQATLPWAICQPEWENCVPSD-PTLAASVNNI 192	237 MMLALAGLPIFFLEVSLGQFASQGPVSVWKAIPALQGCGIAMLIISVLIAIYYNVIICYT 296	95 IVLLLVGKPVYYLECVEGQFSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLC 154	177 ATTTIPEDEQGDENKARGNWSSKLDFILSMVGYAVGLGNVWRFPYLAFQNGGGAFLIPYL 236	35 ALDNIDDTDLEAEPPERNVNSNNIEFLMSCIATSVGLGNVWRFPEIAYQNGGGAFLVPYV 94	Query Match 32.1%; Score 1076.5; DB 2; Length 799; Best Local Similarity 37.5%; Pred. No. 1.1e-74; Matches 224; Conservative 307; Mismatches 228; Indels 39; Gaps 10;	

502

442

560

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C; Superfamily: gamma-aminobutyric acid transporter
C; Keywords: glycoprotein; leucine zipper; phosphoprotein; pro
F; 46-65, Domain: transmembrane #status predicted <TM1>
F; 73-93/Domain: transmembrane #status predicted <TM2>
F; 76-97/Region: leucine zipper motif
F; 117-137/Domain: transmembrane #status predicted <TM4>
F; 217-236/Domain: transmembrane #status predicted <TM4>
F; 242-264/Domain: transmembrane #status predicted <TM6>
F; 242-264/Domain: transmembrane #status predicted <TM6>
F; 232-345/Domain: transmembrane #status predicted <TM7>
F; 374-397/Domain: transmembrane #status predicted <TM8>
F; 374-397/Domain: transmembrane #status predicted <TM9>
F; 457-479/Domain: transmembrane #status predicted <TM9>
F; 457-479/Domain: transmembrane #status predicted <TM10>
F; 500-519/Domain: transmembrane #status predicted <TM11>
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JH0674
L-proline transport protein - rat
L-proline transport protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
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Neuron 8, 915-926, 1992
A;Title: Molecular cloning and expression of a high affinity A;Reference number: JH0674; MUID:92265305; PMID:1350201
A;Accession: JH0674
A;Molecule type: mRNA
A;Residues: 1-637 <FRE>
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                                                                                                                    LPGATDGILFFVTPQWAKLLELGVWYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDA
                                                                                                                                                                                 QI-GRPGEIRWNLCLCLLLAWVIVFLCILKGVKSSGKVVYFTATFPYLILLMLLVRGVT
                                                                                                                                                                                                                                                                                                                    MSFQATLPWAICQPEW--ENCV----PSDPTLAASVNNITNGTSSAQLYFLRTVL--QQS
                                                                                                                                                                                                                                                                                                                                                                                                     VGKPYYYLECYLGQFSSRNSYKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLA
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FIVTLGNAITSILAGFAIFSVLGYMSQELGVPV-DQVAKAGPGLAFVIYPQAMTMLPLSP
                                         WIVTTLDTFTSFLSGCTIFGILGNLAYELNSEVGDVVGAGGTSLAFISYPDAIAKTFQPQ
                                                                                       LPGAWKGIQFYLTPQFHHLLSSKVWIEAALQIFYSLGVGFGGLLTFASYNTFHQNIYRDT
                                                                                                                                                                                                                             DGIEGGLGAPIWYLVLCLFIAWLMVFGVVARGVKSSGKAAYFLALFPYVVMITLFITTII
                                                                                                                                                                                                                                                                             ASLTSNLPWEHCGNWWNTERCLEHRGPKDGNGALPL-NLSSTVSPSEEYWSRYVLHIQGS
                                                                                                                                                                                                                                                                                                                                                                       CGIPLFFLELSLGQFSSLGPLAVWKISPLFKGAGAAMLLIVGLVAIYYNMIIAYVLFYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTDLEAE-PPERMVWSNNIEFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1027; DB 2;
Pred. No. 5.3e-71;
0; Mismatches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236;
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<TM8>
<TM10>
<TM110>
<TM112>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
S11073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S11073
R;Nelson, H.; Mandiyan, S.; Nelson, N.
FEBS Lett. 269, 181-184, 1990
A;Title: Cloning of the human brain GABA transporter.
A;Reference number: S11073; MUID:90353567; PMID:2387399
A;Accession: S11073
A;
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N;Alternate names: GABA transport prote
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision
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A; Residues: 1-599 < NEL>
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                                                            AMDAFPRV----PTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFL-VLFCAIS
                                                                                                                                                                                                                               VTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYE
                                                                                                                                                                                                                                                                                                                         VARGVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSCIATSVGLGNVWREPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGQVNGGFESSEPKMEPKRSSQIS-LPPANNKAALDNIDDIDLEAEPPERMVWSNNIEFL
              LVDEYPRLLRNRRELFIAAV-CIISYLIGLSNITQGGIYVFKLFDYYSASGMSLLFLVFF
                                                                                                                                     LNSEVGDVVGAGGTSLAFISYPDAIAKTFQPQLESVLFFLMMSVLGIGSSVALLSTFNTL 419
                                                                                                                                                                                                                                                                                               {\tt IWKGVGWTGKVVYFSATYPYIMLIILFFRGVTLPGAKEGILFYITPNFRKLSDSEVWLDA}
                                                                                                                                                                                                                                                                                                                                                                                           SN----YSMVNTTNMTSAVVEFWERNMHQMTDGLDKP-GQIRWPLAITLAIAWILVYFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VWKLAPMEKGVGLAAAVLSFWLNIYXIVIISWAIXYLYNSFTTTLPWKQCDNPWNTDRCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEW--ENCV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPGGQYILELVDHYGGTFLVLFCAISELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCW
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                                                                                                             TKRSIAD-VAASGPGLAFLAYPEAVTQLPISPLWAILFFSMLLMLGIDSQFCTVEGFITA
                                                                                                                                                                                                       ATQIFFSYGLGLGSLIALGSYNSFHNNVYRDSIIVCCINSCTSMFAGFVIFSIVGFMAHV
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protein
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Pred. No. 8.3e-70;
8; Mismatches 229
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R;Guastella, J.; Nelson, N.; Nelson, H.; Czyzyk, L.; Keynan, S.; Science 249, 1303-1306, 1990
A;Title: Cloning and expression of a rat brain GABA transporter.
A;Reference number: A35918; MUID:90378307; PMID:1975955
A;Accession: A35918
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F;375-394/Domain:
F;427-447/Domain:
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F;292-312/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: brain; glycoprotein; phosphoprotein; tran: F;53-73/Domain: transmembrane #status predicted <TM1> F;80-100/Domain: transmembrane #status predicted <TM2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: GABA transporter
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
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A; Residues: 546-551; 556-562; 564-566; 572-583
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A; Accession: B35918
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A; Residues: 1-599 < GUA>
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                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                     IWKGVGWTGKVVYFSATYPYIMLIILFFRGVTLPGAKEGILFYITPNFRKLSDSEVWLDA
                                                                                            SN----YSLVNTTNMTSAVVEFWERNMHQMTDGLDKP-GQIRWPLAITLAIAWVLVYFC
                                                                                                                                                                   VWKLAPMFKGVGLAAAVLSFWLNIYYIVIISWAIYYLYNSFTTTLPWKQCDNPWNTDRCF
                                                                                                                                                                                                    VWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEW--ENCV 179
                                                                                                                                                                                                                                          MSCVGYAIGLGNVWRFPYLCGKNGGGAFLIPYFLTLIFAGVPLFLLECSLGQYTSIGGLG
                                                                                                                                                                                                                                                                               MSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GP 589
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R;Swanson, G.T.; Umbach, J.A.; Gundersen, C.B.
J. Neurochem. 63, 1-12, 1994
A;Title: Glia of the cholinergic electromotor nucleus
A;Reference number: 151368; MUID:94267441; PMID:820741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma-aminobutyric acid transport protein GAT-1 - Pacific electric ray
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
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C; Superfamily:
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A; Residues: 1-598 <SWA>
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A;Experimental source: placental trophoblastic cell line JAR A;Experimental source: placental trophoblastic cell line JAR A;Note: sequence extracted from NCBI backbone (NCBIN:128282, 1 Lesch, K.P.; Wolozin, B.L.; Estler, H.C.; Murphy, D.L.; Ried J. Neural Transm. 91, 67-72, 1993

A;Title: Isolation of a cDNA encoding the human brain serotoni A;Recession: S37688

A;Accession: S37688
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references; GDB:134713; OMIM:182138
A;Map position: 17q11.1-17q12
C;Superfamily; gamma-aminobutyric acid transporter
C;Keywords: transmembrane protein
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A;Title: Antidepressant- and cocaine-sensitive human serotonin transparence number: A47398; MUID:93211998; PMID:7681602
A;Accession: A47398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serotonin transporter - human
N;Alternate names: 5-hydroxytryptamine transporter
C;Species: Homo sapiens (man)
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C;Accession: A47398; S37688
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A; Note: the authors translated th
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A; Residues: 1-630 <LES>
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A; Residues: 1-630 < RAM>
A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                     Similarity
-NCVPSDPTLAASVNNIT---NGTSSAQLYFLRTVLQ--QSDGIEGGLGAPIWYLVLCLF
                                                                                                                               CISIWRKICPIFKGIGYAICIIAFYIASYYNTIMAWALYYLISSFTDQLPWTSCKNSWNT
                                                                                                                                                                                                   DFLLSVIGYAVDLGNVWRFPYICYQNGGGAFLLPYTIMAIFGGIPLFYMELALGQYHRNG
                                                                                                                                                                                                                                    EFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRN
                                                                                                                                                                                                                                                                          VESGQISNGY-SAVPSPGAGDDTRHSIPATT------
                                                                                                                                                                                                                                                                                                            MNDGQVNGGFESSEPKMEPKRSSQISLPPANNKAALDNIDDTDLEAE--PPERMVWSNNI 58
                                                     GNC----TNYFSEDNITWTLHSTSPAEEFYTRHVLQIHRSKGLQ-DLGGISWQLALCIM
                                                                                                                                                                 SVKVW-SISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEWE- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIRPIAD-VAASGPGLAFLAYPEAVTQLPISPLWSILFFSMLLMLGIDSQFCTVEGFIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRT--GTFSETIK 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALVDEFPKLLRGRREIFI-AMVCIVSYLIGLSNITQGGLYVFKLFDYYSASGMSLLFLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAMDAFPRV----PTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFL-VLFCAI 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SYIFPKWGQGVGWFMALSSMMLIP---GYMGYMFLTSKGSLKQRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FETVSISWCYGVNRFFVNIEEMVGHKPCLWWKLCWSFFTPIIVGGVFLFSAIQMKPLKMG
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                       29.5%;
37.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NID:g36432;
he codon GGA
                                                                                                                                                                                                                                                                                                                                                                     Score 991; DB 2
Pred. No. 3e-68;
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:CAA50029.1; PID:g36433 for residue 25 as Val and G
                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain serotonin
                                                                                                                                                                                                                                                                                                                                                  24.2;
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                                                                                                                                                                                                                                                                            -TTLVAELHQGERETWGKKV
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 as Val and GAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID: 9291820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transporter:
                                                                                                                                                                                                                                                                                                                                                  46;
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A; Residues: 1-630 <MAY>
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Best Local
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                                                                                                                                                                                                                                                                                                        QVNGGFESSEPKMEPKRSSQISLPPANNKAALDNIDDTDLEAE--PPERMVWSNNIEFLM 62
                                                                                                                                                                                                                                                           W-SISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEWE--NCV 179
                                                                                       VIYFSIWKGVKTSGKVVWVTATFPYIVLSVLLVRGATLPGAWRGVVFYLKPNWQKLLETG
                                                                                                              WVFGVVARGVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELG
::: : :|||:|| : | | ||||| : |
                                                                                                                                                                                    PSDPTLAASVNNIT---NGTSSAQLYFLRTVLQ--QSDGIEGGLGAPIWYLVLCLFIAWL
                                                                                                                                                                                                                                      WRKICPIFKGIGYAICIIAFYIASYYNTIIAWALYYLISSLTDRLPWTSCTNSWNTGNC-
                                                                                                                                                                                                                                                                                                                                                                                  QISNGY-SAVPSTSAGDEASHSIPAAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LELGVWYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIFTVIYESIWKGVKTSGKVVWVTATFPYIILSVLLVRGATLPGAWRGVLFYLKPNWQKL
                   VWVDAAAQIFFSLGPGFGVLLAFASYNKFNNNCYQDALVTSVVNCMTSFVSGFVIFTVLG
                                                   VWYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LASNNL-VFGDNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPAVLTVALIEAVAVSWFYGITQFCRDVKEMLGFSPGWFWRICWVAISPLFLLFIICSFL
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                                                                                                                                                               ---TNYFAQDNITWTLHSTSPAEEFYLRHVLQIHQSKGLQ-DLGTISWQLTLCIVLIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSPPQLRLF--QYNYPYWSIILGYCIGTSSFICIPTYIAYRLI-ITPGTFKERIIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFLVLFCAISELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLSTENTLAMDAFPRV-----PTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.2%;
37.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 981; DB 2;
Pred. No. 1.8e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  ----TTLVAEIRQGERETWGKKMDFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           241;
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20-Aug-1999

610

497 464 380

557 524

46;

Gaps

90

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RESULT 8
$46260

State: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 2
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 2
C;Accession: $46260
R;Guimbal, C.; Kilimann, M.W.
J. Mol. Biol. 241, 317-324, 1994
A;Title: A creatine transporter cDNA from Torpedo illustrates str
A;Reference number: $46260; MUID:94334996; PMID:8057375
A;Accession: $46260
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-611 <GUIT>
A;Cross-references: GB:X77306; NID:g541753; PIDN:CAA54512.1; PID:
C;Superfamily: gamma-aminobutyric acid transporter
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Best Local
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                               LVDHY--GGTFLVLFCAISELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAI
                                                                     CLGLGSQFVGVEGFVTAILDLWPSKFSFRYLREVVVAMVICLSFLIDLSMITEGGMYIFQ
                                                                                                           VLGIGSSVALLSTFNTLAMDAFP-----RVPTVYMSAMTCSCGFLLGLVYCTPGGQYILE
                                                                                                                                               FFAGLVVFSILGFMAVEEGVDI-SVVAESGPGLAFIAYPKAVTLMPFPQVWAVLFFIMLL
                                                                                                                                                                         FLSGCTIFGILGNLAYELNSEVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMS 402
                                                                                                                                                                                                                        LQPDWGKLGEAQVWIDAGTQIFFSYAIGLGTLTALGSYNQLHNDCYKDAFILSLVNSATS
                                                                                                                                                                                                                                                    VTPQWAKLLELGVWYSAVTQVFFSLTVCTGPIINFSSYNGFRHNIYRDAWIVTTLDTFTS
                                                                                                                                                                                                                                                                                                  WELTLCLTATWMLVYFCIWKGVKTSGKVVYVTATFPYIILVILLVRGVTLHGAVQGIVYY
                                                                                                                                                                                                                                                                                                                          WYLVLCLFIAWLMVFGVVARGVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFF
                                                                                                                                                                                                                                                                                                                                                                                                              PWAICQPEWENCVPSDPTLAASVNNITNGTSSAQ----LYFLRTVLQQSDGIEGGLGAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LECVLGQFSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPPERMVWSNNIEFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYY
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IFDYYSASGTTL-LWTAFWECVAVAWVYGGDRYLDDLAWMLGYRPWALVKWCWSVITPLV
                                                                                                                                                                                                                                                                                                                                                                              PWASCNNTWNTAACYEAGANAS-TEIYPPTAPAQSSIVQFWERRVLRLSSGL-GDVGEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEISLGQFMKAGGINAWNIAPLFKGLGYASMVIVFFCNTYYILVLTWSSFYLVQSFSSPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NL-VFGDNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPSW
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Pred. No. 2.4e-67;
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A;Note: sequence extracted from NCBI backbone (NCBIN:112460, C;Superfamily: gamma-aminobutyric acid transporter C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Liu, Q.R.; Mandiyan, S.; Nelson, H.; Nelson, N.
Proc. Natl. Acad. Sci. U.S.A. 89, 6639-6643, 1992
A;Title: A family of genes encoding neurotransmitter transporters.
A;Reference number: A46027; MUID:92335351; PMID:1631167
A;Accession: F46027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma-aminobutyric acid transporter - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C;Accession: F46027
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A;Molecule type: DNA
A;Residues: 1-598 <LIU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 VWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEW--ENCV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 MSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 DGQI-----STEVSEAPVASDKPKTLVVKVQKKAGDLPDRDTWKGRFDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 DGQVNGGFESSEPKMEPKRSSQIS-LPPANNKAALDNIDDTDLEAEPPERMVWSNNIEFL
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                                             NYVYPTAGYVSGYLMLELGMTEVPIGIGESLYKYRT--GTFSETIKKAFHS-----KPSW
                                                                                                                                                                               AMDAFPRV----PTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFL-VLFCAIS:|:|:||:|:||:|::|:||:|::||
                                                                                                                                                                                                                                    TKRSTAD-VAASGPGLAFLAYPEAVTQLPISPLWAILFFSMLLMLGIDSQFCTVEGFITA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SN-----YSLVNTTNMTSAVVEFWERNMHQMTDGLD--KPGQIRCLAITLAIAWVLVYFC
         SYVFPKWGQGVGWLMALSSMVLIP----GYMAYMFLTLKGSLKQRLQVMIQPSEDIVRPEN
                                                                                                                     ELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGD 534
                                                                                                                                                             LVDEYPRLLRNRRELFIAAV-CIVSYLIGLSNITQGGIYVFKLFDYYSASGMSLLFLVFF
                                                                                                                                                                                                                                                                                                                                                                                      IWKGVGWTGKVVYFSATYPYIMLIILFFRGVTLPGAKEGILFYITPNFRKLSDSEVIFDA
                                                                                   ECVSISWFYGVNRFYDNIQEMVGSRPCIWWKLCWSFFTPIIVAGVFLFSAVQMTPLTMG-
                                                                                                                                                                                                                                                                        LNSEVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTL 419
                                                                                                                                                                                                                                                                                                                ATQIFFSYGLGLGSLIALGSYNSFHNNVYRDSIIVCCINSCTSMFAGFVIFSIVGFMAHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSCVGYAIGLGNVWRFPYLCGKNGGGAFLIPYFLTLIFAGVPLFLLECSLGQYTSIGGLG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIKKAFHSKPSWGPRSPRERREWMQFKAEAKALRQKMNTSRVKHLWYSITGA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CMGIFTFHLVNYKPLTYNKTYTYPWWGEAIGWCLALASMLCVPTTVLYSLSRGR-GSLKE
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Pred. No. 2.6e-67;
3; Mismatches 232;
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J. Biol. Chem. 267, 21098-21104, 1992
A;Title: Molecular heterogeneity of the gamma-aminobutyric acid (GABA) transport system. A;Reference number: A45078; MUID:93016029; PMID:1400419
A;Accession: B45078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuron 9, 337-348, 1992
A;Title: Functional expression and CNS distribution of a beta-alanine-sensitive
A;Reference number: JH0695; MUID:92360310; PMID:1497897
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C;Accession: JH0695; B45078
R;Clark, J.A.; Deutch, A.Y.; Gallipoli, P.Z.; Amara, S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma-aminobutyric acid transporter protein 3 - rat
N;Alternate names: GABA transporter 3; gamma-aminobutyric acid transport protein
C;Species: Rattus norvegicus (Norway rat)
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A; Residues: 1-627 <BOR>
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1,433-451/Domain: transmembrane #status predicted <TM9>
1,468-488/Domain: transmembrane #status predicted <T10>
1,509-528/Domain: transmembrane #status predicted <T11>
1,548-566/Domain: transmembrane #status predicted <T12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: gamma-aminobutyric acid transporter (Keywords: brain; glycoprotein; phosphoprotein; trans, 54-74/Domain: transmembrane #status predicted (TMI)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                  SVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVKVW-SIS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPRSPR
GTKSTGKVVYVTATFPYIMLLILLIRGVTLPGASEGIKEYLYPDLSRLSDPQVWVDAGTQ
                                          GVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSAVTQ 302
                                                                                    NFSNYSHVSLQNATSPVMEFWERRVLAISDGIE-HIGNLRWELALCLLAAWTICYFCIWK
                                                                                                                             LAASVNNIT--NGTSSAQLYFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGVVAR
                                                                                                                                                                         PLFEGIGYATQVIEAHLNVYYIIILAWAIFYLSNCFTTELPWATCGHEWNTEKCVEFQKL 181
                                                                                                                                                                                                                  PAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEW--ENCVPSDPT
                                                                                                                                                                                                                                                                                                                                               TAEQALPLGNGKAAEEARGSEALGGGGGGAAGTREARDKAVHERGHWNNKVEFVLSVAGE
                                                                                                                                                                                                                                                                                                                                                                                       SSQISLPPANNKAALDNIDDTDL------EAEPP---ERMVWSNNIEFLMSCIAT
                                                                                                                                                                                                                                                            IIGLGNVWRFPYLCYKNGGGAFLIPYVVFFICCGIPVFFLETALGQFTSEGGITCWRRVC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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#status predicted <TM7>
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predicted <TM4>
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.2e-67;
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A; Residues: 1-635 <MAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett. 305,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;483-500/Domain:
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Best Local S
Matches 209
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                                                                                                                                                                                                                                                                                                                                        SSQISLPPANNKAALDNIDDTDLEAEPPERMVWSNNIEFLMSCIATSVGLGNVWRFPFIA 81
                                                                                                                                                                         YILSYYVVICGLCLYYLAMSFQATLPWAICQPEWE---NCVP---SDPTLAASVNNIT---
                                                                                                                                                                                                                    YKNGGGVFLIPYVLIALVGGIPIFFLEISLGQFMKAGSINVWNICPLFKGLGYASMVIVF 142
                                                                                                                                                                                                                                                                                                         SSRLAVPP-
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                                                                                --NGTSSAQLYFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGVVARGVKSSGKAA 251
                                                                                                                               YCNTYYIMVLAWGFYYLVKSFTTTLPWATCGHTWNTPDCVEIFRHEDCANASLANLTCDQ
                                            LADRRSPVIEFWENKVLRLSTGLEVP-GALNWEVTLCLLACWVLVYFCVWKGVKSTGKIV 261
  YFLALFPYVVMITLFITTIILPGÄTDGILFFVTPQWAKLLELGVWYSAVTQVFFSLTVCT
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-RETWIROMDFIMSCVGFAVGLGNVWRFPYLC

193

311

141

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A; Title: Primary structure and functional expression of a A; Reference number: S23431; MUID:92339519; PMID:1633856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                choline transport protein - rat
C:Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                           F;342-366/Domain: transmembrane #status
F;396-415/Domain: transmembrane #status
                                                                                                                                                                                                                  F;260-277/Domain: transmembrane F;313-330/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                  F;61-83/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                   C;Superfamily: gamma-aminobutyric acid transpor
C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Date: 04-Dec-1992 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: X66494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDN 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFPRV------PTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGT-FLVLFCAISE 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIAE-VAESGPGLAFIAYPKAVTMMPLSPLWATLFFMMLIFLGLDSQFVCVESLVTAVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMD 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTYPAWGYGIGWLMALSSMLCIPLWIFIKLWK-TEGTLPEKLQK 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYPKVFRRGYRRELLILALSI-VSYFLGLVMLTEGGMYIFQLFDSYAASGMCLLFVAIFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKK 579
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35.8%;
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c acid transporter
                                                                                                                                           #status
Score 972; DB 2;
Pred. No. 8.7e-67;
3; Mismatches 228
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RESULT 12
S19585
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C;Superfamily: gamma-aminobutyric acid transporter
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S19585
R;Blakely, R.D.; Berson, H.E.; Fremeau Jr., R.T.
Nature 354, 66-70, 1991
A;Title: Cloning and expression of a functional
A;Reference number: S19585; MUID:92049754; PMID:
A;Accession: S19585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serotonin transport protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Feb-1997
C;Accession: S19585
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A; Residues: 1-607 <BLA>
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                                                                                                                                                           LFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSAVTQVFFSLTVCTGPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLPPANNKAALDNIDDTDLEAE--PPERMVWSNNIEFLMSCIATSVGLGNVWRFPFIAYQ
                                                                                                                                                                                                                            SAQLYFLRTVLQ--QSDGIEGGLGAPIWYLVLCLFIAWLMVFGVVARGVKSSGKAAYFLA
                                                                                                                                                                                                                                                                                                           ILSYYVVICGLCLYYLAMSFQATLPWAICQPEWE--NCVPSDPTLAASVNNIT---NGTS
                                                                                                                                                                                                                                                                                                                                               NGGGAFLLPYTIMAIFGGIPLFYMELALGQYHRNGCISIWRKICPIFKGIGYAICIIAFY
                                                                                                                                                                                                                                                                                                                                                                                 NGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVKVW-SISPAMKGTGYAQAAGCGY
                                                                                                                                                                                                                                                                                                                                                                                                                    SIPAAT-----TTLVAEIRQGERETWGKKMDFLLSVIGYAVDLGNIWRFPYICYQ
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                                    AFISYPDAIAKTFQPQLESVLFFLMMSVLGIGSSVALLSTFNTLAMDAFPRVPT-----
                                                                    AFASYNKFNNNCYQDALVTSVVNCMTSFVSGFVIFTVLGYMAEMRNEDVSEVAKDAGPSL
                                                                                                     MFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNSEVGDVVGAGGTSL
                                                                                                                                         TFPYIVLSVLLVRGATLPGAWRGVVFYLKPNWQKLLETGVWVDAAAQIFFSLGPGFGVLL
                                                                                                                                                                                                           PAEEFYLRHVLQIHQSKGLQ-DLGTISWQLTLCIVLIFTVIYFSIWKGVKTSGKVVWVTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADREMDDIACMIGYRPCPWMKWCWSFETPLVCMGIFIFNVVYYKPLVYNNTYVYPWWGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQREISVALCCALCFVIDLSMVTDGGMYVFQLFDYYSASGTTL-LWQAFWECVVVAWVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPGLAFIAYPRAVTLMPVAPLWAALFFFMLLLLGLDSQFVGVEGFITGLLDLLPASYYFR
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; Pred. No. 9e-6
89; Mismatches
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PMID:1944572
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9e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:SLC6A8; CT-1
A;Cross-references: GDB:434311; OMIM:600394
A;Map position: Xq28-Xq28
A;Introns: 88/1; 132/1; 215/2; 259/3; 304/3; 339/2; 381/1; 418/3; 464/3; 499/1; 532/3
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TPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTG
                                                                                                                                                                                                        TFTSFLSGCTIFGILGNLAYELNSEVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFF
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                                                                  YILELVDHY--GGTFLVLFCAISELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVI
                                                                                                                                   LMMSVLGIGSSVALLSTFNTLAMDAFP-----RVPTVYMSAMTCSCGFLLGLVYCTPGGQ 453
                                                                                                                                                                                                                                                                                                                                                                               ATCGHTWNTPDCVEIFRHEDCANASLANLTCDQLADRRSPVIEFWENKVLRLSGGLEVP-
                                                                                                                                                                                                                                                                                                                                                                                                              AICQPEWE--NCVP---SDPTLAASVNNIT----NGTSSAQLYFLRTVLQQSDGIEGGL
                                YVFQLFDYYSASGTTL-LWQAFWECVVVAWVYGADRFMDDIACMIGYRPCPWMKWCWSFF
                                                                                                     FMLLLLGLDSQFVGVEGFITGLLDLLPASYYFRFQREISVALCCALCFVIDLSMVTDGGM
                                                                                                                                                                       SGTSFFAGFVVFSILGFMAAEQGVHISK-VAESGPGLAFIAYPRAVTLMPVAPLWAALFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.0%; Score 971.5; DB 2; 37.0%; Pred. No. 9.5e-67; Live 99; Mismatches 229;
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September 1995
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511 467

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F:134-160/Domain: transmembrane #status predicted <TM3>
F:23-252/Domain: transmembrane #status predicted <TM4>
F:233-252/Domain: transmembrane #status predicted <TM5>
F:283-277/Domain: transmembrane #status predicted <TM5>
F:287-307/Region: leucine zipper motif
F:314-329/Domain: transmembrane #status predicted <TM6>
F:343-367/Domain: transmembrane #status predicted <TM6>
F:343-367/Domain: transmembrane #status predicted <TM8>
F:445-462/Domain: transmembrane #status predicted <TM9>
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F;520-544/Domain: transmembrane #status predicted <TM11>
F;550-583/Domain: transmembrane #status predicted <TM12>
F;563-583/Domain: transmembrane #status predicted <TM12>
F;54/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predict F;192,197,548/Binding site: carbohydrate (Asn) (covalent) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted F;256/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
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A; Residues: 1-635 <SOR>
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A;Title: The cloning and expression of a human creatine A;Reference number: JC2386; MUID:95032129; PMID:7945388
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SGPGLAFIAYPRAVTLMPVAPLWAALFFFMLLLLGLDSQFVGVEGFITGLLDLLPASYYF
                                                   GGTSLAFISYPDAIAKTEQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMDAFP----
                                                                                                                                                      TGPIIMESSYNGFRHNIYRDAWIVTTLDTETSFLSGCTIFGILGNLAYELNSEVGDVVGA
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                                                                                                      LGALTALGSYNRFNNNCYKDAIILALINSGTSFFAGFVVFSILGFMATEQGVHISK-VAE
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Pred. No. 1e-66;
4; Mismatches 229
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A46061
Na(+)-dependent creatine transporter - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994
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A; Residues: 1-635 <GUI>
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7; Mismatches 232;
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RVPTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHY--GGTFLVLFCAISELAGVFWIY AMGWAFALSSMLCVPLHLLGCLLRAK-GTMAERWQHL--TQPIWG VSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPSWG GLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGY 543 GADREMDDIACMIGYRPCPWMKWCWSFETPLVCMGIFIFNVVYYEPLVYNNTYVYPWWGE REQREISVALCCALCEVIDLSMVTDGGMYVEQLEDYYSASGTTL-LWQAEWECVVVAWVY 588 600 498 483

R;Guimbal, C.; Kilimann, M.W.
J. Biol. Chem. 268, 8418-8421, 1993
A;Title: A Na(+)-dependent creatine transporter in rabbit A;Reference number: A46061; MUID:93231984; PMID:8473283
A;Accession: A46061 A;Experimental source: brain and muscle A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:129571, | C;Superfamily: gamma-aminobutyric acid transporter #text_change brain, NCBIP: 129580) muscle, heart, and

YILELVDHY--GGTFLVLFCAISELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVI TPLVCMGIFIFNIVYYKPLVYNKTYVYPWWGEAMGWAFALSSMLCVPLHLLGCLLRAK-G TPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTG 571 ILFFVTPQWAKLLELGVWYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLD GAPIWYLVLCLFIAWLMVFGVVARGVKSSGKAAYFLALFPYVVMITLFITTIILPGATDG CVLGQFSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPW 168 YVFQLFDYYSASGTTL-LWQAFWECVAVAWVYGADRFMDDIACMIGYRPCPWMKWCWSFF FMLLLLGLDSQFVGVEGFITGLLDLLPASYYFRFQREISVALCCALCFVIDLSMVTDGGM LMMSVLGIGSSVALLSTENTLAMDAEP-----RVPTVYMSAMTCSCGFLLGLVYCTPGGQ SGTSFFAGEVVFSILGFMATEQGVHISK-VAESGPGLAFIAYPRAVTLMPVAPLWAALFF TFTSFLSGCTIFGILGNLAYELNSEVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFF GALNWEYTLCLLACWYLYYFCYWKGYKSTGKIYYFTATFPYYYLYYLLYRGYLLPGALDG ATCGHTWNTPDCVEIFRHEDCANGSLANLTCDQLAERRSPVIEFWENKVLRLSGGLEVP-AICQPEWE--NCVP---SDPTLAASVNNIT----NGTSSAQLYFLRTVLQQSDGIEGGL ISLGQFMKAGSINVWNICPLFKGLGYASMVIVFYCNTYYIMVLAWGFYYLVKSFTTTLPW IIYYLKPDWSKLRSPQVWIDAGTQIFFSYAIGLGALTALGSYNRFNNNCYKDAIILALIN 109 108 453 467 407 398 348 338 278 228 218 169 288

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P51905 drosophila
035899 cavia porce
P31641 homo sapien
P48067 mus musculu
P31650 mus musculu
P31640 mus musculu
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P48056 rattus norv
P31648 mus musculu
P48066 homo sapien
O18875 bos taurus
O9mz34 bos taurus
P31647 rattus norv
P28570 rattus norv
P48029 homo sapien
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FAMILY (SNF).	hal cord and cerebellum.	ECIFICITY: 1	strychnine-sensitive glycinergic synapses.	reuptake into presynaptic terminals. May be termination of neurotransmission at	ites the action of glycine by its high aff	uuman glycine type 2 transporter.)6/1999)	tion and	Cairns W., O	MEDLINE=20074920; PubMed=10606742;	SEQUENCE FROM N.A., AND VARIANTS ARG-184; ASN-463 AND ALA-751.	ed (JAN-1999) to the EMBL/GenBank/DDBJ databases.	and everteesion of a human clustee transporter tupe it a	SEQUENCE FROM N.A.	Brain Res. Mol. Brain Res. 70:101-115(1999).	"Characterization of multiple forms of the human glycine transporter type-2".	16; PubMed=10381548;	SEQUENCE FROM N.A.	FEBS Lett. 439:334-340(1998). [2]	GlyT2 and chromosomal localisation of the gen ne.";	cloning and functional expression of the hu	, Collie I.T., Dunbar	oubMed=984534	ID=9606;	etazoa; theria;	(Human	chloride-dependent glycine trans	n e	88; Q9 (Rel.	6A5_HUMAN STANDARD; F	OUT 1	ALIGNMENTS	20	931.5 27.8 614 1 S6AC_RABIT P48055	933 27.8 619 1 S6AS_RAT P23977	935 27.9 633 I S6A6_RAT 934.5 27.9 621 1 S6A6_MOUSE	935 27.9 633 1 S6A9_MOUSE P28571 mus mus	936 27.9 615 1 SGA2_BOURN P51143 bos	940.5 28.0 614 1 S6AC_CANFA P27799 cani
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AF117999; AAK12641.1;
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PROSITE; PS00754;
PROSITE; PS50267;
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Symport.
                     Neurotransmitter transport;
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                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long a
modified and this statement is not removed;
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sodium- and chloride-dependent glycine transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Liu Q.-R., Lopez-Corcuera B., Mandiyan S., Nelson H., Nelson "Cloning and expression of a spinal cord- and brain-specific transporter with novel structural features.";

J. Biol. Chem. 268:22802-22808(1993).

J. FUCTION: Terminates the action of glycine by its high af sodium-dependent reuptake into presynaptic terminals. May responsible for the termination of neurotransmission at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94043045;
                                                                                                                                                                                                              Pfam; PF00209;
                                                                                                                                                                                                                                                                                                   EMBL; L21672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
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                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Specifically expressed in spinal cord, b:
stem, and to a lesser extent in the cerebellum.
SIMILARITY: BELONGS TO THE SODIUM: NEUROTRANSMITTER SYMPORTER
FAMILY (SNF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strychnine-sensitive glycinergic synapses.
SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262
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IPRO00175; Na/ntran_sympc
9209; SNF; 1.
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NA_NEUROTRAN_SYMP_3;
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Sciurognathi; Muridae;
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                                                                                                                               EPPKYLRTHKPVFTLGCCICFFIMGFPMITQGGIYMFQLVDTYAASYALVIIAIFELVGI
                                                                                                                                                                                                     VFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNS
                                                                                                                                                                                                                          GVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSAVTQ
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                                                                     NWSMVLGWLMLACSVIWIPIMFVIKMY-LAPGRFIERLKLVCSPQPDWGPFLAQHRGE
                                                                                  TAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPSWGPRSPRERRE
                                                                                                          FWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYP
                                                                                                                                         AFPRVPTVYMSAMT---CSCGFLLGLVYCTPGGQYILLELVDHYGGTFLVLFCAISELAGV
                                                                                                                                                               NIENVADQ.
                                                                                                                                                                       EVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMD
                                                                                                                                                                                                                                                         TMVNFTSQANKTFVSGSEEYFKYFVLKISAGIEYP-GEIRWPLPFCLFLAWVIVYASLAK
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87908 MW;
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                                STANDARD;
24, Created)
40, Last sequence up
40, Last annotation
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Pred. No. 1.3
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                        86
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- I- FUNCTION: TERMINATES THE ACTION OF PROLINE BY IT SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMI- I- SUBCELLULAR LOCATION: Integral membrane protein - ITSSUE SPECIFICITY: EXPRESSED IN SUBPOPULATIONS GLUTAMATERGIC PATHWAYS OF RAT BRAIN.
- I- SIMILARITY: BELONGS TO THE SODIUM: NEUROTRANSMITT FAMILY (SNF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0176; NANEUSMPORT.

ProDom; PD000448; NA/ntran_Symport; 1.

PROSITE; PS00610; NA_NEUROTRAN_SYMP_1;

PROSITE; PS00754; NA_NEUROTRAN_SYMP_3;

PROSITE; PS50267; NA_NEUROTRAN_SYMP_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-92265305; PubMed-1350201; Fremeau R.T. Jr., Caron M.G., Blakel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sodium-dependent proline SLC6A7.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuron 8:915-926(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
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                                                                                                                                                                                                       Similarity
MSFQATLPWAICQPEW--ENCV----PSDPTLAASVNNITNGTSSAQLYFLRTVL--
                                   CGIPLFFLELSLGQFSSLGPLAVWKISPLFKGAGAAMLLIVGLVAIYYNMIIAYVLFYLF
                                                        VGKPVYYLECVLGQFSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLA
                                                                                                           DVDLDVDFAADRGNWTGKLDFLLSCIGYCVGLGNVWRFPYRAYTNGGGAFLVPYFLMLAI
                                                                                                                                 DTDLEAE-PPERMVWSNNIEFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transport;
                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                182
71090
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expression of a high affinity L-proline
in putative glutamatergic pathways of rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transporter
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11 (POTENTIAL).

12 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (PO
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Pred. No. 1.9e
90; Mismatches
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3 (POTENTIAL).
EXTRACELLULAR (
4 (POTENTIAL).
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6 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
8 (POTENTIAL).
9 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SODIUM: NEUROTRANSMITTER SYMPORTER
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l.9e-60;
nes 236;
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S6A7_L
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                       Genew; HGNC:
MIM; 606205;
                                   EMBL; S80071; AAB47007.2;
Genew; HGNC:11054; SLC6A7
                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                 Shafqat S., Velaz-Faircloth M., Henzi V.A., Whitney K.I. Yang-Peng T.L., Seldin M.F., Fremeau R.T., Jr.; "Human brain-specific L-proline transporter: molecular functional expression, and chromosomal localization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
16-OCT-2001 (Rel. 40,
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Q99884;
                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                         FUNCTION: TERMINATES THE ACTION OF PROLINE BY ITS H
SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINAL
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: BRAIN.
SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER
                                                                                                                                                                                                                              FAMILY (SNF)
                                                                                                                                                                                                                                                                                                                                 n and mouse genomes.";
Pharmacol. 48:219-229(1995)
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IPR000175; Na/ntran_symport
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Primates;
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PROSITE; PS00610;
PROSITE; PS00754;
PROSITE; PS50267;
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PS00610; NA_NEUROTRAN_SYMP_1;
PS00754; NA_NEUROTRAN_SYMP_3;
PS50267; NA_NEUROTRAN_SYMP_3;
                                                                                  RTGTFSETIKKAFHSKPSWGPRSPRERREWM
                                                                                                                                                   GVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKY
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12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
L -> V (IN DESNP:1468564).
FTId-VAR_011390.
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EXTRACELLULAR
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
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Pred. No. 5.4e-60;
7; Mismatches 239
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P30531;
01-APR-1993
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16-OCT-2001 (Rel. 40, Last annotation update)
Sodium- and chloride-dependent GABA transporter
SLC6A1 OR GABATR OR GABT1 OR GAT1.
                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are
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Eukaryota; Metazoa;
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ProDom; PD000448; Na/ntran_symport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson H., Mandiyan S., Nelson N.;
"Cloning of the human brain GABA transporter.";
FEBS Lett. 269:181-184(1990).
                                                                           CARBOHYD
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Neurotransmitter transport; Transport;
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                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
                      Local 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: TERMINATES THE ACTION OF GABA BY ITS HIGH AFFIN SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS. SUBCELLULAR LOCATION: Integral membrane protein.
MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
SIMILARITY: BELONGS TO THE SODIUM: NEUROTRANSMITTER SYMPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAMILY (SNF)
                                                                                                                                                                                                                                                                                                                                          137165;
                                                                                                                                                                                                                                                                                                                                                            S11073; S11073
                                                                                                                                                                                                                                                                                                                       PF00209;
                                                                                                                                                                                                                                                                                                                                                  HGNC:11042; SLC6A1.
           ω
                                     Similarity
                                                                                                                                                                                                                                                     Multigene
                                                                                                                                                                                                                                                                                PS00754; NA_NEUROTRAN_SYMP_2;
         DGQVNGGFESSEPKMEPKRSSQIS-LPPANNKAALDNIDDTDLEAEPPERMVWSNNIEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Metazoa; Chordata;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                              IPR000175; Na/ntran_symport.
                                                                                              145
212
2212
239
292
292
321
375
422
457
457
457
536
                             Conservative
                                                                                                                                                                                                                                                                                                                       SNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                             440
477
517
554
599
176
181
181
184
67014
                                                                                                                                                                                                                                                                                         NA_NEUROTRAN_SYMP
                                                                                                                                                                                   100
144
211
230
256
                                                                                                                                                                                                                                                     family.
                                     30.1%;
35.4%;
                            118;
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                                                            10 (POTENTIAL).

11 (POTENTIAL).

12 (POTENTIAL).

12 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (GLUNAC...) (POTENTIAL).

N-LINKED (GLUNAC...) (POTENTIAL).

N-LINKED (GLUNAC...) (POTENTIAL).

245CB39C19315D08 CRC64;
                                                                                                                                         CYTOPLASMIC (POTENTIAL).

1 (POTENTIAL).

2 (POTENTIAL).

3 (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

7 (POTENTIAL).

8 (POTENTIAL).

9 (POTENTIAL).
                       Pred. No. 2e 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            599
                                                                                                                                                                                                                                                            ; 1.
; 1.
; Transmembrane;
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                                                                           (POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
                                                                                                                                                                                                                                                              Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                           and
                          42;
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S6A1_R
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96A1_RAT STANDARD; PR: P23978 (Rel. 21, Created) 01-MAR-1992 (Rel. 21, Last seque) 16-OCT-2001 (Rel. 40, Last annots Sodium - and chloride-dependent GSCGLC6A1 OR GABT1 OR GAT-1.
            J. Biol. Chem. 272:14695-14704(1997).
                                                                               MEDLINE=97313439;
Clark J.A.;
                                                                                                                                                 "Cloning and expression of a rat Science 249:1303-1306(1990).
                                                                                                                                                                                               Guastella J.,
                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                 Miedel M.C.,
                                                                                                                                                                                                                  MEDLINE=90378307; PubMed=1975955;
                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
 SODIUM-DEPENDENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRT--GTFSETIKKAFHS----KPSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECVSISWEYGVREYDNIQEMVGSRPCIWMKLCWSFETPIIVAGVFIFSAVQMTPLTMG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVDEYPRLLRNRRELFIAAV-CIISYLIGLSNITQGGIYVFKLFDYYSASGMSLLFLVFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMDAFPRV----PTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFL-VLFCAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKRSIAD-VAASGPGLAFLAYPEAVTQLPISPLWAILFFSMLLMLGIDSQFCTVEGFITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IWKGVGWTGKVVYFSATYPYIMLIILFFRGVTLPGAKEGILFYITPNFRKLSDSEVWLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SN-----YSMYNTTNMTSAVVEFWERNMHQMTDGLDKP-GQIRWPLAITLAIAWILVYFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSDPTLAASVNNITNGTSSAQLYFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VWKLAPMFKGVGLAAAVLSFWLNIYYIVIISWAIYYLYNSFTTTLPWKQCDNPWNTDRCF
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(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      589
                                                                                                                                                                                 Davidson N.,
                                                                                                                                                                                                 Nelson
                                                                                                  PubMed=9269433;
                                                                                                                                                                                                                                                                                                                                 (Rat).
                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
ATES THE ACTION OF GABA BY REUPTAKE INTO PRESYNAPTIC
                                                                                                                                                                                                 N., Nelson H.,
                                                                                                                                                                Lester H.A., Kanner B.I.;
a rat brain GABA transporter.";
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                                                                                                                                                                                                                                                                                                  Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                  GABA transporter
                                                                                                                                                                                               Czyzyk L., Keynan
                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    599
                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                   Vertebrata;
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                                                                                                                                                                                                                                                                                                   Muridae;
 TERMINALS
                 HIGH
                                                                                                                                                                                                                                                                                                                     Euteleostomi;
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                                                                                                                                                                                                                                                                                                   Murinae; Rattus.
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                 AFFINITY
                                                                 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466
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Matches
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PRODOM; PD000448; Na/ntran_symport; 1.
PROSITE; PS00610; NA_NEUROTRAN_SYMP_1;
PROSITE; PS00754; NA_NEUROTRAN_SYMP_3;
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Symport;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M59742;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e by non-profit institutions as long as its content is in no way diffed and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restropean profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein.
MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHC
STIMULANTS SUCH AS AMPHETAMINES OR COCALINE.
SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY (SNF).
                                                 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A35918;
                                                                   55
                                                                                     62
                                                                                                        10
                                                                                                                                           Similarity 34.8
11; Conservative
PSDPTLAASVNNITNGTSSAQLYFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMYFGV
                                          VWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEW--ENCV
                                                                MSCVGYAIGLGNVWRFPYLCGKNGGGAFLIPYFLTLIFAGVPLFLLECSLGQYTSIGGLG
                                                                            MSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVK 121
                                                                                                                       DGQVNGGFESSEPKMEPKRSSQIS-LPPANNKAALDNIDDTDLEAEPPERMVWSNNIEFL
                           VWKLAPMFKGVGLAAAVLSFWLNIYYIVIISWAIYYLYNSFTTTLPWKQCDNPWNTDRCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000175; Na/ntran_symport.
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                                                                                                                                                                                184
67001
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                                                                                                                                                    30.1%;
                                                                                                                                            122;
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                                                                                                                                          Score 1008; D
Pred. No. 3.1e
22; Mismatches
                                                                                                                                                                                                                                                                        EXTRACELLULAR (PROBABLE).
8 (PROBABLE).
CYTOPLASMIC (PROBABLE).
9 (PROBABLE).
EXTRACELLULAR (PROBABLE).
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2 (PROBABLE).
CYTOPLASMIC (PROBABLE).
3 (PROBABLE).
EXTRACELLULAR (PROBABLE).
                                                                                                      STEVSEAPVASDKPKTLVVKVQKKAGDLPDRDTWKGRFDFL
                                                                                                                                                                                                                                                                                                                                                             4 (PROBABLE).
CYTOPLASMIC (
5 (PROBABLE).
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CYTOPLASMIC (F
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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12 (PROBABLE).
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1 (PROBABLE).
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ches 231;
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                                                                                                                                                                                                                                                                                                                                                                     (PROBABLE).
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                                                                                                                                                           Length 599;
                                                                                                                                           Indels
                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
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RESULT 7
S6A4_MACMU
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similarity).
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
-i- MISCELLANEOUS: THIS PROTEIN OR COCAINE (By similarity).
-i- SIMILARITY: BELONGS TO THE SODIUM: NEUROTRANSMITTER SYMPORTER
                                                                                                                     Miller G.M., Yatin S.M., De La Garza R. II, Goulet M., Ma "Cloning of dopamine, norepinephrine and serotonin transp monkey brain: relevance to cocaine sensitivity."; Brain Res. MOl. Brain Res. 87:124-143(201).

-I- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta (Rhesus macaque).
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15-JUN-2002
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use by non-profit institutions as low modified and this statement is not removementities requires a license agreement (SC or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restr EMBL; AF285761; InterPro; IPR002437; IPR000175; AAF97247.1; institutions as long as its content atement is not removed. Usage by an Na/ntran_symport 5HT_transporter (See http://www. There are no restrictions isb-sib and EMBL is of for a collaboration outstation

FAMILY (SNF).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00754;
KPSWGPRSPRE 594
                                                  GPAVLTVALIEAVAVSWFYGITQFCRDVKEMLGFSPGWFWRICWVAISPLFLLFIICSFL
                                                                 TFLVLFCAISELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYAL
                                                                                                 ALLSTFNTLAMDAFPRVPT-----VYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGG
                                                                                                                  TVLGYMAEMRNEDVSEVAKDAGPSLLFITYAEAIANMPASTFFAIIFFLMLITLGLDSTF
                                                                                                                                                    LETGVWIDAAAQIFFSLGPGFGVLLAFASYNKFNNNCYQDALVTSVVNCMTSFVSGFVIF
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                 MSPPQLRLF--QYNYPHWSIILGYCIGTSSFYCIPTYIAYRLIS-TPGTFKERIIK----
                                                                                  AGLEGVITAVLDEFPHIWAKRREWFVLAVVITCFFGSLVTLTF--
                               LASNNL-VFGDNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHS
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5HT_transporter;
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NA_NEUROTRAN_SYMP_1;
NA_NEUROTRAN_SYMP_2;
NA_NEUROTRAN_SYMP_3;
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4 (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

7 (POTENTIAL).

8 (POTENTIAL).

9 (POTENTIAL).
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12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . . ) (P
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; Transmembrane; (
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L.5e-58;
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         RESULT 8
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- FUNCTION: TERMINATES THE ACTION OF GABA BY ITS HIGH AFFIR SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.

- SUBCELLULAR LOCATION: Integral membrane protein.

- TISSUE SPECIFICITY: BRAIN.

- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.

- SIMILARITY: BELONGS TO THE SODIUM: NEUROTRANSMITTER SYMPOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sodium- and chloride-dependent GABA transporter
SLC6A1 OR GABTIOR GAT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                         Prodom; PD000448; NA_ntran_symport; 1
PROSITE; PS00610; NA_NEUROTRAN_SYMP_1;
PROSITE; PS00754; NA_NEUROTRAN_SYMP_2;
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; LFRU
Pfam; PF00209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95049273; PubMed=7960586; Ruiz M., Egal H., Sarthy V.P., Qian X.J., "Cloning, expression, and localization of aminobutyric acid transporter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S6A1_MUSCO P48057;
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ProDom; PD000448; Na/ntran_symport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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0209; SNF;
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66783
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  ¥.
              12 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (P

N-LINKED (GLCNAC. . .) (P

N-LINKED (GLCNAC. . .) (P
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(POTENTIAL).
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Best Local
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    [2]
SEQUENCE FROM N.A.
MEDLINE-93211998; PubMe
                                                   MEDLINE-93199744; PubMed-8452685; Lesch K.P., Wolozin B.L., Estler F. Isolation of a cDNA encoding the J. Neural Transm. 91:67-73(1993).
                                                                                                                                                                     Homo
                                                                                                                                                                                                  P31645;
01-JUL-1993 (Rel. 26, Creat
01-JUL-1993 (Rel. 26, Last
16-OCT-2001 (Rel. 40, Last
                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                              Sodium-dependent serotonin SLC6A4 OR HTT OR SERT.
                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                                                                                                                                 S6A4_HUMAN
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                                                                                                               SEQUENCE
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                 PubMed=7681602;
                                                                                                                                             Chordata;
Primates;
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34
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          A.L.,
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                                                                                                                                                                                         transporter
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          K.R.,
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                                                                                                                                                                                       transporter) (5HTT).
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        Η.,
                                                               D.L., Ried
serotonin
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        Yang-Feng
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                                                                          Riederer P.;
                                                                                                                                                        Euteleostom1
                                                                transporter.";
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Best Local S
Matches 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang A.S., Ganapathy V., Blakely R.D.;
"Antidepressant- and cocaine-sensitive human serotonin transporter:
molecular cloning, expression, and chromosomal localization.";
Proc. Natl. Acad. Sci. U.S.A. 90:2542-2546(1993).
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X70697; CAA50029.1; -.
EMBL; U5568, AAA33492.1; -.
EMBL; U79746; AAB93475.1; -.
PIR; S37688; S37688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradley C.C., Blakely Submitted (JUN-1997)
Local 226;
                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                   Pfam; PF00209; SNF; 1.
Pfam; PF03491; 5HT_transporter;
                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S37688;
PIR; A47398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93260476; Pu
Lesch K.P., Wolozin
                                                    SEQUENCE
                                                               CARBOHYD
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InterPro; IPR000175; Na/ntran_symport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93260476; PubMed=7684072;
Lesch K.P., Wolozin B.L., Murphy D.L., Reiderer P.;
"Primary structure of the human platelet serotonin
identity with the brain serotonin transporter.";
J. Neurochem. 60:2319-2322(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Platelet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitted (JUN-1997) to the EMBL/GenBank/DDBJ databases. FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH AFFINITY SODDIUM-DEDENDEMT REOPTAKE INTO PRESYNAPTIC TERMINALS SUBCELLALARE INCATION: Integral membrane protein. SUBCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
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                                                                                                                                                                                                                                                                                                                                                                                          HGNC:11050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (S an email to license@isb-sib.ch).
                 Similarity
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                                                                                                                                                                                                                                                                              PS00754;
PS50267;
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     Conservative
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                                                   A
                                                                                                                                                                                                                                                                 transport;
                                                                                                                                                                                                                                                                             NA_NEUROTRAN_SYMP_2;
NA_NEUROTRAN_SYMP_3;
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NA_NEUROTRAN_SYMP
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37.0%;
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                                                           6 (POTENTIAL).
7 (POTENTIAL).
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9 (POTENTIAL).
10 (POTENTIAL).
11 (POTENTIAL).
12 (POTENTIAL).
CYTOPLASNIC (POTENTIAL).
CYTOPLASNIC (POTENTIAL).
N-LINKED (GLCNAC...) (F
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1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
EXTRACELLULAR
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                 Score
Pred.
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                                                   0EB535B0A579BDA2 CRC64;
       Mismatches
                          991;
                 No. 4.3e-58
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                             DВ
                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
                          Length 630;
       Indels
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                                                            (POTENTIAL)
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RESULT 10
SCA4_MOUSE
ID SCA4A
AC Q6085
DT 15-JU
DT 15-JU
DT 16-OC
DE SOGIU
GN SLC6A
OC MUS II
RN [1]
RN [1]
RN SEQUI
RX MEDLI
RA Chana
RA MEDLI
RA Chana
RA MEDLI
RA SEQUI
RA MEDLI
RA 
                                                                                                                                                                                                                                                                                                                                              SGA4_MOUSE STANDARD; PRT; 63
G08857; O35241;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence upd
16-OCT-2001 (Rel. 40, Last annotation u
Sodium-dependent serotonin transporter
SLC6A4 OR HTT OR SET.
                                                                                                                                                                                            Chang
                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
                  MEDLINE=97225900; PubMed=9073170;
Bengel D., Heils A., Petri S., Seemann
Murphy D.L., Lesch K.P.;
                                                                                                                                                                            Chang A.S.,
Blakely R.D
                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-97189261;
                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                 STRAIN-129;
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                          *Cloning and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
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    structure and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIFTVIYESIWKGVKTSGKVVWVTATFPYIILSVLLVRGATLPGAWRGVLFYLKPNWQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNDGQVNGGFESSEPKMEPKRSSQISLPPANNKAALDNIDDTDLEAE--PPERMVWSNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SITPETPTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPAYLTVALIEAVAVSWFYGITQFCRDVKEMLGFSPGWFWRICWVAISPLFLLFIICSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVLGYMAEMRNEDVSEVAKDAGPSLLFITYAEAIANMPASTFFAIIFFLMLITLGLDSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GILGNLAYELNSEVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LETGVWIDAAAQIFFSLGPGFGVLLAFASYNKFNNNCYQDALVTSVVNCMTSFVSGFVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LELGVWYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAWLMVFGVVARGVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -NCVPSDPTLAASVNNIT---NGTSSAQLYFLRTVLQ--QSDGIEGGLGAPIWYLVLCLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CISIWRKICPIFKGIGYAICIIAFYIASYYNTIMAWALYYLISSFTDQLPWTSCKNSWNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFLLSVIGYAVDLGNVWRFPYICYQNGGGAFLLPYTIMAIFGGIPLFYMELALGQYHRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VESGQISNGY-SAVPSPGAGDDTRHSIPATT-----TTLVAELHQGERETWGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPSWGPRSPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSPPQLRLF --QYNYPYWSIILGYCIGTSSFICIPTYIAYRLI-ITPGTFKERIIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LASNNL-VFGDNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFLVLFCAISELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGLEGYITAVLDEFPHVWAKRRERFVLAVVITCFFGSLVTLTF---GGAYVVKLLEEYAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALLSTFNTLAMDAFPRV-----PTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGG
                                                                                                                                       Mol.
                                                                                                                                                                                              Chang S.M.,
                                                                                                                                       Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TNYFSEDNITWTLHSTSPAEEFYTRHVLQIHRSKGLQ-DLGGISWQLALCIM
                                                                                                                                                                                                                   PubMed=9037532;
                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
    5'-flanking regulatory region of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              594
                                                                                                                                                        of
                                                                                                                                                                                              Starnes
                                                                                                                                     the mouse serotonin 43:185-192(1996).
                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                              D.M.,
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                                        M., Glatz
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                                                                                                                                                                                                                                                                                              Muridae;
                                                                                                                                                                                                                                                                                                                                                                         transporter)
                                                                                                                                                          transporter.";
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                                                                                                                                                                                                Bauman
                                                                                                                                                                                                                                                                                              Murinae;
                                          Andrews
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Ъ δ 밁 Qy 밁 Qy В δÃ

δõ 밁 γQ 밁 Ş ₽ ô 밁 δ B Ω 밁 Q

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Saito N.,
Ikegaki N.
                                                 MARIM. Genome 4:283-284(1993).

1 FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH
AFFIRITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS

1 SUBCELLULAR LOCATION: Integral membrane protein.

1 MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.

1 SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
                                                                                                                                                                                                                                                                                                                                                                                                      Brain
[3]
                                                                                                                                                                                                               MEDLINE=93283858; PubM
Gregor P., Patel A., S
Seldin M.F., Uhl G.R.;
                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-
STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                     serotonin transporter.";
Brain Res. Mol. Brain Res. 44:286-292(1997).
                                                                                                                                                                                 chromosome 11."
                                                                                                                                                                                                                                                                          SEQUENCE OF 69-630
                                                                                                                                                                                                Murine serotonin transporter: sequence and
CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT FRAMESHIFT IN POSITION 195.
                                    FAMILY (SNF)
                                                                                                                                                                                                                                                                                                                                                                                   OF 1-114 FROM N.A
                                                                                                                                                                                                                                                                                                                                               Sakai N., Kobayashi
                                                                                                                                                                                                                                                                                                            (MAY-1995)
                                                                                                                                                                                                                                                     PubMed=8507984;
                                                                                                                                                                                                                                                                          FROM
                                                                                                                                                                                                                                                                                                            ţ
                                                                                                                                                                                                                                      Shimada
                                                                                                                                                                                                                                                                          N.A
                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                      s.
                                                                                                                                                                                                                                                                                                                                               s.,
                                                                                                                                                                                                                                      Lin
                                                                                                                                                                                                                                                                                                                                               Fujimoto M.,
                                                                                                                                                                                                                                      C.L.,
                                                                                                                                                                                                                                      Rochelle J.M.,
                                                                                                                                                                                                    localization
                   SHOWN
                                                                                                                                                                                                                                                                                                              databases
                                                                                                                                                                                                                                                                                                                                                  Morikawa
                   DUE
                                                                                                                                                                                                                                                                                                                                                  0
                   TO
                                                                                                                             TERMINALS
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                                                                                                                                                                                                                                      Kitayama
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TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                        Symport.
                                                                                                                                                                                                                                                       EMBL;
EMBL;
EMBL;
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EMBL;
EMBL;
EMBL;
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         TRANSMEM TRANSMEM
                                                                                        TRANSMEM TRANSMEM
                                                                                                                                                    PRINTS; PRO0176; NANEUSMPORT.

PRODOM; PD000448; NA_Ntran_symport; 1.

PROSITE; PS00610; NA_NEUROTRAN_SYMP_1;

PROSITE; PS00754; NA_NEUROTRAN_SYMP_3;

PROSITE; PS50267; NA_NEUROTRAN_SYMP_3;
                                                                                                                                                                                                    Pfam; PF00209; SNF; 1.
Pfam; PF03491; 5HT_transporter; 1.
                                                                                                                                                                                                                                              MGD;
                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                            TRANSMEM
                                                                                                                                          Neurotransmitter
                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                          InterPro;
TRANSMEM
                              FRANSMEM
                                       TRANSMEM
                                                                                                                                                                                                                        MGI:96285; Slc6a4.
rPro; IPR002437; 5H
rPro; IPR000175; Na
                                                                                                                                                                                                                                                                                                Y08876; CAA70092
Y08877; CAA70092
Y08878; CAA70092
                                                                                                                                                                                                                                                       U26452; AAA84750.
X66119; -; NOT_AN
                                                                                                                                                                                                                                                                                                                             Y08874; CAA70092.1;
Y08875; CAA70092.1;
                                                                                                                                                                                                                                                                                      Y08879; CAA70092
                                                                                                                                                                                                                                                                                                                                                  Y08872; CAA70092.
Y08873; CAA70092.
                                                                                                                                                                                                                                                                                                                                                                    Y08870; CAA70092.1;
Y08871; CAA70092.1;
                                                                                                                                                                                                                                                                            Y08880;
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88
116
160
181
253
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280
333
362
417
464
498
                                                                                                                                                                                                                                                                            CAA70092
                                                                                                                                                                                                                                                     NOT_ANNOTATED_CDS
                                                                                                                                          transport;
87
108
135
136
252
271
271
297
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436
482
558
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                                                                                                                                                                                                                                    5HT_transporter
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                                                                                                                                                                                                                                                                                                                                                                      JOINED
                                                                                                                                         Transport;
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9
11
                                                                                EXTRACELLULAR
                                                                                                                       CYTOPLASMIC
                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                        (POTENTIAL)
                                                                                                            (POTENTIAL)
                    (POTENTIAL)
         (POTENTIAL)
                                                                                                                                          Transmembrane;
                                                                                                                       (POTENTIAL)
                                                                                 (POTENTIAL).
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Glycoprotein;

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RESULT 11
S6A4_BOVII
ID 4_BOVII
ID 4_BOVII
ID 6A4_AC Q9XT4
AC Q9XT4
AC Q9XT4
DT 16-00
DT 16-00
DT 16-00
DT Scd11
GN SLC61
OS BOS 1-1
OC Manna
OC Manna
OC MOBI
RP SEQU
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Best Local S
Matches 228
                                                                             16-OCT-2001 (Rel. 40, Create 16-OCT-2001 (Rel. 40, Last s 16-OCT-2001 (Rel. 40, Last a sodium-dependent serotonin t SLC6A4 OR SERT.
                                                                                                                                             S6A4_BOVIN
Q9XT49;
                Bos taurus (Bovine).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;

Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
SEQUENCE FROM N.A
                                                                                                                                                                      BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSCIATSVGLGNVWREPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQISNGY-SAVPSTSAGDEAPHSTPAAT-----TTLVAEIHQGERETWGKKMDFL
                                                                                                                                                                                                                                          WGPRSPRE
                                                                                                                                                                                                                                                                                                                                                                                                                      GVWVDAAAQIFFSLGPGFGVLLAFASYNKFNNNCYQDALVTSVVNCMTSFVSGFVIFTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIIYFSIWKGVKTSGKVVWVTATFPYIVLSVLLVRGATLPGAWRGVVFYLKPNWQKLLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VW-SISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEWE--NC
                                                                                                                                                                                                                   ITPETPTE 619
                                                                                                                                                                                                                                                               PQLRLF--QYNYPHWSIILGYCIGTSSVICIPIYIIYRLIS-TPGTLKERIIK-----
                                                                                                                                                                                                                                                                                     NNL-VFGDNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPS
                                                                                                                                                                                                                                                                                                           VLTVALIEAVVVSWFYGITQFCSDVKEMLGFSPGWFWRICWVAISPLFLLFIICSFLMSP
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CYTOPLASMIC (POTENTIAL)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
P -> Q (IN REF. 2).
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Pred. No. 4.3e-58;
5; Mismatches 239;
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                                                                                                                                                        PRT;
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-> R (IN REF. 2).
F37EF1EC1764FB30 CRC64;
                                                                                                                                                       630
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(POTENTIAL).
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                                             Bovoidea;
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CARBOHYD
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TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                 Symport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00209; SNF; 1.
Pfam; PF03491; 5HT_transporter; 1.
PRINTS; PR00176; NANEUSMPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00610; PROSITE; PS00754; PROSITE; PS50267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF119122; AAD26262.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serotonin transporter. ;
Brain Res. Mol. Brain Res. 71:120-126(1999).
-i- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS
AFFINITY SODIUM-DEPENDENT REUTIAKE INTO PRESYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002437; 5HT_transporter.
InterPro; IPR000175; Na/ntran_symport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
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"Molecular cloning, expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99337805; PubMed-10407194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, BRAIN STEM, BR
MARROW, KIDNEY, LUNG, HEART, ADRENAL GLAND, LIVER, PARATI
GLAND, THYROID GLAND, SMALL INTESTINE AND PANCREAS.
MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
STINULANTS SUCH AS AMPHETAMINES OR COCAINE.
SIMILARITY: BELONGS TO THE SODIUM: NEUROTRANSMITTER SYMPOI
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                                                                                             PPERMYWSNNIEFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYL
              PWAICQPEWE --
                                   ELALGQYHRNGCISIWTKICPIFKGIGCAICLIAFYIASYYNTIIAWALYYLISSFTEQL
                                                                                  PAERETWAKKVDFLLSVIGYAVDLGNVWRFPYICYQNGGGAFLLPYTIMAIFGGIPLFYM
                                                                                                                                                         DGQVNGGFESSEPKMEPK-RSSQISLPPANNKAALDNI---DDTD---
                                                          ECVLGQFSSRNSVKVWS-ISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATL
                                                                                                                                DCQENGVLQKGVPAPGDKAESGQIS----NGYSAVPNPGAGDDTQHSIPAATTALVAEVH
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.NA_NEUROTRAN_SYMP_3;
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NA_NEUROTRAN_SYMP_1;
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NCVPSDPTLAASVNNIT---NGTSSAQLYFLRTVLQ--QSDGIEGGLG
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11 (POTENTIAL).

12 (POTENTIAL).

12 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transport;
                                                                                                                                                                                         Score 987; DB 1;
Pred. No. 7.9e-58;
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                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 1.
; 1.
; Transmembrane; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
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SEQUENCE FROM N.A.

MEDLINE=92054541; PubMed=1948036;
Hoffman B.J., Mezey E., Brownstein M
"Cloning of a serotonin transporter
Science 254:579-580(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P31652; P23976;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 12
_RAT
                                                                                                                                                                                                                                                                                       Prince H.K., Bardley C. "Cloning and expression rat brain.";
                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain stem;
MEDLINE=92049754; PubMed=1944572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mayser W., Betz H., Schloss P., "Isolation of cDNAs encoding a novel transporter gene family.", FEBS Lett. 295:203-206(1991).
                                                                                                                                                                             TISSUE=Brain stem;
Blakely R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLC6A4.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                    Blakely R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92111740; PubMed=1765155;
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                                                                                                                                                    (JUL-1992) to
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                                                                                                                                                                                                                                                                                                                               Bardley C.C.;
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Rodentia;
                                                                                                                                                      the
                                         Brownstein M.J.;
transporter affected
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annotation update)
transporter (5HT transporter)
                                                                                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                        functional
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                     bу
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                                     antidepressants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                 Peek
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Best Local
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH
AFFINITY SODIUM-DEPENDENT RECUTAKE INTO PRESYNAPTIC TERMINALS.
-I- SUBCELLOLAR LOCATION: Integral membrane protein.
-I- SUBCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
-I- SIMILARITY: BELONGS TO THE SODIUM: NEUROTRANSMITTER SYMPORTER
                                                                                                                   SEQUENCE
                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X63995; CAA45401.1;
EMBL; X63253; CAA44913.1;
EMBL; M79450; AAA42186.1;
EMBL; Y11024; CAA71909.1;
                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                               TRANSMEN
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ProDom; PD000448; Na/ntran_symport;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00209; SNF; 1.
Pfam; PF03491; 5HT_transporter; 1.
                                                                                                                                                                                                                                                                                         TRANSMEN
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                                                                                                                                                                                                                                                                                                                                                     Symport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                  Neurotransmitter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ween the Swiss Institute of Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY (SNF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $30604; $30604.
$19585; $19585.
           63
                                42
                                                    5
                                                                                    Similarity
SCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVKV 122
                              QISNGY-SAVPSTSAGDEASHSIPAAT
                                         PS00610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002437;
IPR000175;
                                                                                                                  630
                                                                         Conservative
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                                                                                                                  ΑĄ;
                                                                                                                                                                                                                                                                                                                                                              transport;
                                                                                                                                                                                                                                                                                                                                                                         Na/ntran_symport; 1.
Na_NEUROTRAN_SYMP_1;
NA_NEUROTRAN_SYMP_2;
NA_NEUROTRAN_SYMP_3;
                                                                                                                                      87
108
135
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272
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37.2%;
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                                                                         94;
                                                                                                                                                               10 (POTENTIAL).
11 (POTENTIAL).
12 (POTENTIAL).
12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (F
                                                                                                                                                                                                                                                       EXTRACELLULAR
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                Transport;
                                                                      Score 981; DB 1;
Pred. No. 2e-57;
1; Mismatches 241
                                                                                                                KPTGLLL (IN REF. 4)
44DA7C5888C403EE
                                                                                                                                  A -> G (IN REF. 4).
PGWF -> GMV (IN REF. 4).
PCGDIRMNAV -> RVGHPHECCVTHPGRGHLFPATSLSSE
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                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no
                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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                            -TTLVAEIRQGERETWGKKMDFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             its content
                                                                                         Length 630
                                                                                                                 CRC64;
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                                                                      46;
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                                                                     Gaps
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DP Pd

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SVIGYAVDLGNIWRFPYICYQNGGGAFLLPYTIMAIFGGIPLFYMELALGQYHRNGCISI W-SISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEWE--NCV

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P48056;
01-FEB-1996 (Rel. 33, Create
01-FEB-1998 (Rel. 36, Last s
15-JUL-1998 (Rel. 36, Last s
Sodium - and chloride-depende
betaine/GABA transporter).
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Biochim.
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE-97019277; PubMed-8865807; Burnham C.E., Buerk B., Schmidt C., Bucuvalas "A liver-specific isoform of the betaine/GABA
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                A sequence and organ distribution.";
chim. Blophys. Acta 1284:4-8 (1996).
EUNCTION: TRANSPORTS BETAINE AND GABA. MAY HAVE A ROLE IN
REGULATION OF GABAERGIC TRANSMISSION IN THE BRAIN THROUGH
REUPTAKE OF GABA INTO PRESYNAPTIC TERMINALS, AS WELL AS IN
REGULATION (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SUBCELLULAR LOCATION: OTHE SODIUM: NEUROTRANSMITTER SYMPORT
                                                                                                                                                FAMILY (SNF).
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ota; Metazoa; Chordata;
ia; Eutheria; Rodentia;
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(Rel. 33, Last sequence update)
(Rel. 36, Last annotation update)
chloride-dependent betaine transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                     (See http://www.isb-sib.ch/announce/
                                                        There are no restrictions ng as its content is in
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PROSITE; PS00610; Na_NEUROTRAN_SYMP_1;
PROSITE; PS00754; NA_NEUROTRAN_SYMP_3;
PROSITE; PS50267; Na_NEUROTRAN_SYMP_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U28927; AAC52867.1; ALT_INIT: InterPro; IPR000175; Na/ntran_sympo
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . . ) (P
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ID S6AL

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DT 01-JU

DT 01-JU

DT 16-OC

GN SLOGI

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Best Local
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MEDLINE-9235351; PubMed-1631167;

Liu Q.-R., Mandiyan S., Nelson H., Nelson N.;

"A family of genes encoding neurotransmitter transporters.";

PLOC. Natl. Acad. Sci. U.S.A. 89:6639-6643(1992).

-!- FUNCTION: TERMINATES THE ACTION OF GABA BY ITS HIGH AFFINITY

SODIUM-DEPENDENT REUPTAKE INTO PRESYMAPTIC TERMINALS.

-!- SUBCELLUAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: BRAIN.

-!- MISCELLANDOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR

SIMULANTS SUCH AS AMPHETAMINES OR COCAINE.

-!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
                                                                                                               CARBOHYD
                                                                                                                                                                                                                  TRANSMEM
TRANSMEM
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PRODOM: PD000448; Na/ntran_symport; 1.
PROSITE; PS00610; NA_NEUROTRAN_SYMP_2;
PROSITE; PS00754; NA_NEUROTRAN_SYMP_3;
Neurotransmitter transport; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P31648;
Ol-JUL-1993 (Rel. 26, Created)
Ol-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sodium- and chloride-dependent GABA transporter
SLC6A1 OR GABTI OR GAT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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M92378; -; NOT_ANNOTATED_CDS.
        Similarity
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0209; SNF; 1.
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        29.2%;
34.3%;
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2 (POTENTIAL).
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6 (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
Score 978.5; DB 1
Pred. No. 2.7e-57;
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                     '1'
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                     Length 598;
                                                                                 (POTENTIAL)
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RESULT 15

S6AB_HUMAN

ID S6AB_H
AC P48066

DT 01-FEB
OC Mammal
OX NCBL_T
RN [1]
RP SEQUEN
RC TISSUE
RX MEDLIN
RA Borden
RA Glucho
RA Glucho
RT FCloni
RI Identi
RL Recept
CC -i-FU
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CC -i-SU
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SEQUENCE FACE.

TISSUE-FERTAL brain;

REDLINE-95179472; PubMed-7874447;

Borden L.A., Murali Dhar T.G., Smith K.E., Branchek T.A.,

Gluchowski C., Weinshank R.L.;

"Cloning of the human homologue of the GABA transporter GAT-3 and identification of a novel inhibitor with selectivity for this sit Recept. Channels 2:207-213(1994).

-i-FUNCTION: TERMINATES THE ACTION OF GABA BY ITS HIGH AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.

"TOTALLITAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                               P48066;
01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
16-CCT-2001 (Rel.
Sodium- and chlori
SLCGAll OR GABT3 C
                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                    S6AB_HUMAN
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(Rel. 40, Last annotation update)
Chloride-dependent GABA transporter
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PRODOM; PD000448; NA_NEUROTRAN_SYMP_1;
PROSITE; PS00610; NA_NEUROTRAN_SYMP_2;
PROSITE; PS00754; NA_NEUROTRAN_SYMP_3;
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3;
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fam; PF00209; SNF; 1.
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                                                 353
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LGFMAYEQGVPIAE-VAESGPGLAFIAYPKAVTMMPLSPLWATLFEMMLIFLGLDSQFVC
                                              LGNLAYELNSEVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVAL 412
                                                                                                     PQVWVDAGTQIFFSYAICLGCLTALGSYNNYNNNCYRDCIMLCCLNSGTSFVAGFAIFSV
                                                                                                                                                       LGVWYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGI.
                                                                                                                                                                                                              WTICYFCIWKGTKSTGKVVYVTATFPYIMLLILLIRGVTLPGASEGIKFYLYPDLSRLSD
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                                                                                                                                                                                                                                                                                                                                                          -ENCVPSDPTLAASVNNIT--NGTSSAQLYFLRTVLQQSDGIEGGLGAPIWYLVLCLFIA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEFVLSVAGEIIGLGNVWRFPYLCYKNGGGAFLIPYVVFFICCGIPVFFLETALGQFTSE 116
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
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4 (POTENTIAL).
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Db	Qy	Дb	Qy	Db	Qy
534 KYKPLKYNNIYTYPAWGYGIGWLMALSSMLCIPLWICITYWK-TEGTLPEKLQK 586	526 ASNNLVEGDNYVYPTAGYVSGYLMLFLGMTFVPTGIGFSLYKYRTGTFSETIKK 579	474 MCLLFVAIFECICIGMVYGSNRFYDNIEDMIGYRPPSLIKMCMMIMTPGICAGIFIFFLI 533	466 FLVLFCAISELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIWTTVFFYALL 525	415 VESLYTAVVDMYPKVFRRGYRRELLILALSV-ISYFLGLVMLTEGGMYIFQLFDSYAASG 473	413 LSTENTLAMDAEPRVPTVYMSAMTCSCGELLGLVYCTPGGQYILELVDHYGGT- 465
CITVWK-TEGTLPEKLOK 586	FSLYKYRTGTFSETIKK 579	SLIKWCWMIMTPGICAGIFIFFLI 533	AYWRLCWGVITPAIMTTVFFYALL 525	GLVMLTEGGMYIFQLFDSYAASG 473	JGLVYCTPGGQYILELVDHYGGT- 465

Search completed: July 21, 2003, 09:25:20 Job time: 26 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Minimum
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3 drosophila
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Q25512 manduca sex	Q9wtr3 rattus norv	Q8r2i2 mus musculu	Q9r0x6 mus musculu	4 ratt	Q9gjt7 saimiri sci	Q63380 rattus norv	Q9gjt5 saimiri sci	Q9jj41 mus musculu	macaca	gallus	1 mus mu	Q9w1j0 drosophila	Q90zv1 brachydanio	Q91w12 mus musculu	Q9de16 oreochromis	Q91503 torpedo mar		ב	Q8vbwl mus musculu	O42482 rana catesb	Q8vcs9 mus musculu	Q,	Q91502 torpedo mar	О	4 torpedo o	1 raja	Q9un76 homo sapien	3 mus

ALIGNMENTS

Qu Be Ma	R R R R R R R R R R R R R R R R R R R	RESULT 1 Q9U5A9 ID Q9U AC Q9U AC Q9U DT 01- CO C MAIN CO C Ptec OC Sph ON (CA)
Query Match 100.0%; Score 3354; DB 5; Length 633; Best Local Similarity 100.0%; Pred. No. 1.4e-259; Matches 633; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 MNDGQVNGGFESSEPKMEPKRSSQISLPPANNKAALDNIDDTDLEAEPPERMVWSNNIEF 60	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=MIDGUT; MEDLINE=2038/341; Pubmed=10829035; Reldman D.H., Harvey W.R., Stevens B.R.; Feldman D.H., Harvey W.R., Stevens B.R.; Reldman D.H., Harvey W.R., Stevens B.R.; "A novel electrogenic amino acid transporter is activated by K+ or Na+, is alkaline pH-dependent, and is C1independent."; J. Biol. Chem. 275:24518-24526(2000). EMBL; AF013963; AARF18560.1; InterPro; IPR000175; Na/Antran_symport. Pfam; PF00209; SNF; 1. PFAMTS; PR00176; NANEUSMPORT. PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1. PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.	LT 1 A9 A9 A9 Q9U5A9 PRELIMINARY; PRT; 633 AA. Q9U5A9; Q1-MAY-2000 (TrEMBLrel. 13, Created) Q1-MAY-2000 (TrEMBLrel. 21, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update) Amino acid transporter/amino acid-gated channel for sodium/potassium ions. CAATCH1. Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Prerygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea; Sphingidae; Sphinginae; Manduca. NOBI_TaxID=7130;

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01-NOV-1998 (TrEMBLrel 0
01-NOV-1998 (TREMBLrel 0
01-JUN-2002 (TREMBLrel 2
Potassium coupled amino a
KAAT1
                                           Proc. Natl. Acad. Sci. U.S.A. 95:5395-5400(1998)
EMBL; AF006063; AAC24190.1; -
InterPro; IPR000175; Na/ntran_symport.
Pfam; PF00209; SNF; 1.
Pfam; PF00176; NANEUSHPORT.
PRINTS; PR00176; NA/NEUSHPORT.
PRODOm; PD000448; Na/ntran_symport; 1.
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
SEQUENCE 634 AA; 70239 MW; 28EA7A027D240654
                                                                                                                                                                                                                                                                    Manduca sexta (Tobacco hawkmoth) (Tobacco hornwor
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapc
Pterygota; Neoptera; Endopterygota; Lepidoptera;
Sphingiodea; Sphingidae; Sphinginae; Manduca.
NCBI_TaxID=7130;
                                                                                                                                                                                                              Castagna M., Shayakul
                                                                                                                                                                      transporter.";
                                                                                                                                                                                                   Hediger M.A.;
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                                                                                                                                                                                  "Cloning and characterization
      / Match
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hkul C., Trotti
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FKAEAKALRQKMNTSRVKHLWYSITGAYRRNIN
                      WIYGLENLCLDIEFWMGKTTGFYWRLCWGIVTPGMMIIVFIYALLSFENLVFGDFYVYPV
                                                   WIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPT
                                                                     NSEVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTENTLA
                                                                                                                   MNDGQVNGGFESSEPKMEPKRSSQISLPPANNKAALDNIDDTDLEAEPPERMYWSNNIEF
                                                                                                                                                                                                                                         MNDGQVNGGFESSEPKMEPKRSSQISLPPANLKATMDNIDDMDLEAEPPERMVWSNNIEF
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TD Q9W4C5 PRELIMINARY; PRT; 593 AA.

AC Q9W4C5,
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG3252.
GN CG3252.
GN CG3252.
GN CG3252.
GN CG3252.
CS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
GN CFETYYOTA; Metazoa; Arthropoda; Tracheata; Brachycera; Muscomorpha;
CC Eukaryota; Muscomorpha;
CC Eukaryota; M
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Mon

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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Broktein P., Brottier P., RA Burlis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Ra Bolser C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Liu X., Mattei B., Kolira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Liu X., Mattei B., Kolntosh T.C., McLeod M.P., Marris N.L., Ra McIntosh T.C., McLeod M.P., McBreson D., RA Mount S.M., Moly M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., She B.C., Stenlard S., Sunb B.C., Stenlard S., Stupski M.P., Smith T., RA Shue B.C., Siden Kiamos I., Simpson M., Strong R., Sunb E., Spradling A.C., Stapleton M., Strong R., Sunb E., Spier E., Spradling A.C., Stapleton M., Strong R., Sunb E., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Yulliams S.M., Woodage T., Weinstock G.M., Weissenbach J., Ra Zheng X.H., Zhong F.N., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O., Rabic, Emphasion S., Shong M., Strong G., Zhao O., Zheng L., Science 287:185-2195(2000).

Brither C. Branch C. Stapleton M., Strong G., Zhao O., Zheng L., Rhbi, Rabica Emphasion S. Mobin G.M., Venter T., Shon S., Zhu X., Smith H.O., Rhbis R., Shong F.N., Zhong W., Zhou S., Zhu X., Smith H.O., Rhbis R., Shong S., Shong M., Venter J.C.;

Brither C. Stapleton S., Shong M., Venter J.C.;

Brither C. Stapleton S., Shong M., Shong S., Zhu X., Smith H.O., Rhbis R., Shong M., Shong S., Z
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PRODOM; PD000448; NA/Ntran_Symport; 2.

PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.

PROSITE; PS00267; NA_NEUROTRAN_SYMP_3; 1.

PROSITE; PS00267; NA_NEUROTRAN_SYMP_3; 1.

SEQUENCE 593 AA; 66854 MW; 118A6C491F2BFF00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0029762; CG3252.
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                                                                                                                                                                                                                                                     279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IWSVVPGFVGVGVGQAFGTICIISYYSSLLALTLYYLFVSFQSELPWSYCRDEWTNCVNS
                                                                                               | ILFEVTPQWAKLLELGVWYSAVTQVFESLTVCTGPIIMESSYNGFRHNIYRDAWIVTTLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPTLAASVNNITNGT----
                           LFFLMMSVLGTGSSVALLSTFNTLAMDAFPRVFTVYMSAMTCSCGFLLGLVYCTPGGQYI
                                                                                                                                                                                                    ILFFLEPOWGELLNPTVWKEAVVQCFFSLAVGSGPIIMFASYNRFDHGIYRDAMIVTTLD
LEFFMLFVLGIGSIVALQSTIVTIICDQFKGWKYWKVALTTSVCGFLMGLVYVTPGGQWI
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Pred. No. 2.3e-113;
7; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SSAQLYFLRTVLQQSDGIEGGL
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01-DEC-2001
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Stapleton M., Brokstein P., Hong L., Farfan D., Frise E., George Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C., Miranda M., Mungall C., Lewis S.E., Rubin G. M., Celniker S., Phouanenavong S., W. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AY060339; AAL25368.1; FIYBase; FB900339; AAL25368.1; FIYBase; FB900339; Na/ntran_symport. Ffam; PF00209; SNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00209; SNF; 1.
Pfam; PF00209; SNF; 1.
ProDom; PD000448; NA_Ntran_symport; 1.
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
PROSITE; PS50267; NA_NEUROTRAN_SYMP; 4385D/6627C68758 CRC64;
PROSITE; PS504 AA; 72438 MW; 4385D/6627C68758 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
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                                                                                                                                                                                                                       MKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEW-ENCVPSDPTLAA 187
                                                                                                                                                                                                                                                                VGLGNYWREPETAYQNGGGAELVPYYTVLLLYGKPYYYLECYLGQFSSRNSYKVWSISPA 128
                                                                                                                                                                                                                                                                                                                          ESSEPKMEPKRSSQISLPPANNKAALDNIDDTDLEAEPP--ERMVWSNNIEFLMSCIATS
                                                                                                                                                                        SVNNITNG---TSSAQLYFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGVVARGV 244
                                                                                                                                                                                                       KSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSAVTQVF
                                                                                                                                               RATSLAGSGYRTTSAEFYFTNIILREKASIDDGIGYPSWSLALALAVAWIVIAGIMFKGV
VGDVVGAGGTSLAFISYPDAIAK-TFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMD
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48.8%;

    Created)
    Last sequence update)
    Last annotation update)

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pred. No. 2.66
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RA Adams M.D. Cchinker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Bandari D., Bolshakov S., Beense P.V., Bernan B.P., Bhandari D., Bolshakov S., Dables B., Dateley S., Dahlke C., Davenport L.B., Davies P., RA Borkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Gerbios B., Delekr A., Dong S., Mays A.D., Dew I., Dietz S.M., Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W., RA Glodek A., Gong F., Gorriell J.H., Gu Z., Guan P., Harris M., Fleischmann W., RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Harvey D., Helman T.J., Hernandez J.R., Houck J., Jalai M., Kallish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., McInth J., Marris J., McShrefi A., McInth S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Klimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lin X., McShrefi A., McShrefi A., McShrefi A., McShrefi A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Alexacio M., Hishina N.V., Mobarry C., Morist J., Puri V., Reese M.G., Ra Klimel B.C., Schepet S., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., S
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Q9V5B3;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, I
01-JUN-2002 (TrEMBLrel. 21, I
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MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
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ker S.E., Holt R.
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O9VJR4 PRELIMINARY; PRT; 639 AA.

O9VJR4; PRTLIMINARY; PRT; 639 AA.

O1-MAY-2000 (TrEMBLrel. 13, Created)

Prol-MAY-2000 (TrEMBLrel. 13, Last sequence update)

Prol-JUN-2002 (TrEMBLrel. 21, Last annotation update)

BG:DS03431.1 protein (GH16161P).

N BG:DS03431.1 protein (GH16161P).

S BG:DS03431.1 protein (GH16161P).

S Drosophila melanogaster (Fruit fly).

C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;

C Pterygota; Neoptera; Endopterygota; Diptera; Brachyc
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PRINTS; PR00176; Na/ntran_symport; 1.
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
SEQUENCE 651 AA; 72070 MW; 30C81FA13C973285 CRC64;
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"The genome sequence of Drosophila
Science 287:2185-2195(2000).
EMBL; AE003832; AAF58902.1;
FlyBase; FBgn003343; CG1698.
Thterpr. Incondig:
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Pfam; PF00209; SNF; 1.
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                          EWMOFKAE--AKALRQKMNTSRVKHLWYSI
                                                                         GYLMLFLGMTFVPIGIGFSLY------KYRTGTESETIKKAFHSKPSWGPRSPRERR
                                                                                                                KRLCRDVEEMIGIKTSLYYRICWAVVTPLLMLTILIYTLVLYEPLKYKD-YTYQSGVYVF
     RYQLFVQEGNANALFRRSS---
                                                                                                                                    ENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVS
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                                                     -SAFGVGQVLFWAIPAVRKQPSHLGLWAR-IRKAFEPLPNWGPSDPQTLK
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Pred. No. 7
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Tracheata; Hexapoda;

Brachycera;

Muscomorpha.

Insecta;

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RA Abril J.F., Abdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Darvenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Borkova D., Barriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lilang Y., Lin X.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Malson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainzolo M., Pittman G.S., Sanders R.D.C., Scheeler F., Shen H.,
RA Syler E., Spradling A.C., Stapleton M., Skupskin M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupskin M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupskin M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupskin M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Shapson M., Skupskin M.P., Smith T.,
RA Shue B.C., Stapleton M., Strong R., San E.,
RA Shue B.C., Shap R., Rubin G.M., Weissenbach J.,
RA Yells S., Lin S., Shap R., Shap G., Zhao Q.A.,
Par J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A.,
Then J., Shap R., Rubin G.M., Venter J., Shu X., Smith H.O.,
The Shap R., Shap R., Shap R., Shap R., Shap R., Shap R., Shap R
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Sutton G.G., Wortman J.R., Yar
Brandon R.C., Rogers Y.-H.C.,
                                                                                                                                                                                                                                                                                                                                                     Problem; PD000448; Na/ntran_symport; PROSITE; PS50267; Na_NEUROTRAN_SYMP. SEQUENCE 639 AA; 71400 MW; B36Cl
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Amanatides P.G., Scherer S.E., Li P.W.,
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                                                                                                                                                                                                                                                                   Similarity
                                  IAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVKVWSISPAMKGTGYAQAAG
                                                                                                  RSTASTVEISTNSPALRDNSDDQEAAKVPEERATWGKGVEFLMSCIAMSVGLGNVWRFPF
                                                                                                                                                                RSSQISLPPANNKAAL-DNIDDTDLEAEPPERMVWSNNIEFLMSCIATSVGLGNVWRFPF
PubMed=10731132;
                                                                                                                                                                                                                                                               43.9%;
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                                                                                                                                                                                                                                                               Score 1472.5;
Pred. No. 2.76
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2.7e-109;
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----HKEIENELTPKRGQGIW----AAIKQNI
                   FKAEAKALRQKMNTSRVKHLWYSITGAYRRNI
                                                                 WSYSIGWLITAFGILQLPIWMIVAIVRDPGQTLGAKIRGAFTPKKNWGPSDPLLREQY--
                                                                                                 AGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPSWGPRSPRERREWMQ
                                                                                                                                                                                                     RDRFPNFGQWQCSLLIAVVSFFIGLMYITPGGQYMLTLVDFFGASMIALVLGIAELYTIG
                                                                                                                                                                                                                     MDAFPRVPTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGVF
                                                                                                                                                                                                                                                                     DIGSVV-KGGAGLAFISYPDAIAK-FKNLPQIFSVLFFLMLFVLGIGSNIAMTSCSVTAI
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                                                                                                                                                                                                                                                                                                                                                                          FFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNS-
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637
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RESULT

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O Hypothetical 82.8 Now F.

BG:DS03431.1 OR CG15279.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Trache
C Pterygota; Neoptera; Endopterygota; Di

C Pterygota; Neoptera; Endopterygota; Di

--hvdroidea; Drosophilidae; Drosophil Q9NKA8; Q9NKA8; 01-OCT-2000 MEDLINE-99403001; PubMed-104/1/0/;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Ashburner M. Galle R., George R., Harris N., Hartzell G., Harvey D.,
Doyle C., Galle R., George R., Johnson G., Martin C., Moshrefi A.,
Hong L., Houston K., Hoskins R., Johnson G., Wan K., Whitelaw K Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R., Butenhoff C., Champe M., Chavez C., Chew M., Clesiolka L., Doy, Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A., Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee Palazzolo M., Reese M.G., Spradling A., Tsar Celniker S., Rubin G.M.; "An exploration of the sequence of a 2.9-Mb Drosophila melanogaster: the Adh region."; Genetics 153:179-219(1999). 01-OCT-2000 01-JUN-2002 STRAIN-BERKELEY; STRAIN-BERKELEY; SEQUENCE FROM N.A. SEQUENCE FROM N.A. (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TremBLrel. 21, Last annotation update) P., PRELIMINARY; м.а., erygota; Diptera; Drosophila. PRT; Tracheata; Hexapoda; Insecta; . P. 739 region Brachycera; Muscomorpha; of, the Moshrefi M. genome Doyle

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Best Local S
Matches 309
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A Zieran L.L., Rubin G.M.;
L Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. R EMBL; AE003411; AAF44897.1; -
R FiyBase; FB9n0028866; BG:DS03431.1.
R InterPro; IPR000175; Na/ntran_symport.
R Pfam; PF00209; SNF; 1.
R PFAM; PF00209; SNF; 1.
R PRINTS; PR00176; NANGURORT.
R PFAM; PF000448; Na/ntran_symport; 3.
R PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
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                                                                                                  GAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVSGYLMLFLGMTFVPIG
      WYSITGAYRRNI
                            MIVAIVRDPGQTLGAKIRGAFTPKKNWGPSDPLLREQY------KEIENELTPKRGQGI
                                                                                                                            RSSQISLPPANNKAAL-DNIDDTDLEAEPPERMYWSNNIEFLMSCIATSVGLGNVWRFPF
                                                                         AIAKTFQ--PQLFSVLFFLMMSVLGIGSSVALLSTENTLAMDAFPRVPTVYMSAMTCSCG
                                                                                                                                                                                                                                                                                          TLEITTIILPGATDGILFEVTPOWAKLLELGVWYSAVTQVFFSLTVCTGPIIMESSYNGF
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                                                                                                                                                                                                                                                                             VLLVRAVTLPGSIDGIYYFIKPQWGKILDPKVWYAAVTQCFYSLSVCFGNIIMYSSFNKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWA
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                                                   IGFSLYKYRTGTFSETIKKAFHSKPSWGPRSPRERREWMQFKAEAKALRQKMNTSRVKHL
                                                                                                                                                                              AIAK-FKNLPQIFSVLFFLMLFVLGIGSNIAMTSCSVTAIRDRFPNFGQWQCSLLIAVVS
                                                                                                                                                                                                                                                                                                                                                                             ESFRNPLPWSTCRAEWGIHCINSAPDASNWSQLESNDQRPQNYTMKSQNDRVITSSEWYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHRHSVHQLARSCPKYATTSIGVGIGQVISISMVTTYYVAIMGITLRYLYESFRSPLPWS
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42.2%; Pred. No. 2.4e
tive 98; Mismatches
      632
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t., Wan K.H., Weinburg T.,
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T., Zhang
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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Bartin J.E., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Hallew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Hallew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Heson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Ghodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Melneri K.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Moris J., Moshrefi A.,
RA Melneri K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Harris S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Ra Melnert K., Remington K.A., Simpson M., Skupski M.P., Sinth T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
Ra Wells S.M., Moyers E.W., Zhong W., Zhong S., Zho Q., Zheng L.,
RA Jaha S., Zhong T., Robin G.M., Venter 
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Matches 28
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01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                    InterPro; IPRO00175; Na/ntran_symport.
Pfam; PE00209; SNF; 1.
Pfam; PE00209; SNF; 1.
PRINTS; PR00176; NANEUSMPORT.
PRODOM; PD000448; Na/ntran_symport; 2.
PROSITE; PS50267; Na_NEUROTRAN_SYMP_3; 1.
SEQUENCE 629 AA; 69715 MW; F50871F7358BCD5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
SCHENGL, AE003822; AAF58538.1; -.
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0033708; CG8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY
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   56
                                                                                                                                     10
                                                                                                                                                                                                                                   Similarity
NNIEFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFS 115
                                                               YQKLRRNMQGAQGSREGHPGSN-----DGISTVIYSAEGEELTINCEAESESSGQRDQWS
                                                                                                                                 FESSEPKMEPKRSSQISLPPANNKAALDNIDDTDLEAEPPE
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                                                                                                                                                                                                    Score 1414; DB 5;
Pred. No. 1.3e-104;
3; Mismatches 209;
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a; Brachycera; Musc
                                                                                                                                                                                                                                                                   Length 629;
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                                                                                                                                     -RMVWS
                                                                                                                                                                                                    Gaps
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Harris

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K.A.,

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RESULT
OPENSATION
OF THE CONTROL OF 
RP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-BERKELEY;

RX MEDLINE-20196006; PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Gebblos B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VSV2;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG4476 protein.
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHson C., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong X., Zho Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
DR FilyBase, FBgn00359; Cd4476.
DR FilyBase, FBgn003599; Cd4476.
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PRODOM; PD000448; Na/ntran_symport; 1.
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
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InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00209; SNF; 1.
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Harris N.L., Harvey D., Heiman T.J.,
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                              MLVILVYSLLTMRPLSYNGQEFPLVYRVVGWCVSGCI---IGQLF--YWAGYANFKQPKG
                                                                                                                                                                  GVMYFLTPQWEKLLEPQVWYNAVTQVFFSLAVCFGVIIMYSSYNRFGHNVYRDANIVTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GILFFVTPQWAKLLELGVWYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMSFQATLPWAICQPEW-ENCVPSDPTLAASVNNITNGTSSAQLYFLRTVLQQSDGIEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDDTDLEAEPPERMYWSNNIEFLMSCIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLL
                                                                                 MTTVFFYALLASNNLVF-GDNY--VYPTAGY-VSGYLMLFLGMTFVPIGIGFSLYKYRTG
                                                                                                                                      ITLMDFHGVTFVSLVSAIFELIAVGWIYGTKRLCQDAEYMLNIKTSNYYRICWSIVTPLV
                                                                                                                                                                                                                                          LFFAMLFMLGVGSNVGMVSCIMTVLKDQFVNVKLWIIVVSLSVIGFLVGLIYITPGGQHI
                                                                                                                                                                                                                                                                                                                                                                                 DTFTSFLSGCTIFGILGNLAYELNS-EVGDVVGAGGTSLAFISYPDAIAK-TFQPQLFSV
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49.0%;
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Pred. No. 1.1
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OBT7E1;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF369383; AAM13400.1; -. SEQUENCE 615 AA; 68985 MW; E14A5ED2E809A139 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dasher M.K., Kohn A.B., "AeNAAT, A Novel Amino Midgut.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid transporter.
Amino acid transporter.
Aedes aegypti (Yellowfever mosquito).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culi
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                                           QWGPCTEHTRKAWLKYKEEAKSRRDDIIYAKNHSSIVRKL
                                                                                      SWGPRSPRERREWMQFKAEAKALRQ-----KMNTSRVKHL 620
                                                                                                                                                                                                                                           NWCNDIEFMVQRRVGLY--------VAAMLGSNNATFHDCRFHLFLVEYKW.
                                                                                                                                                                                                                                                                                         NLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGD------
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Pred. No. 1.3
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Larval
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21, Glycine transporter type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001920; ASP/GLU_race.
InterPro; IPR000175; Na/ntran_symport.
Pfam; PF00209; SNF; 1.
Pr0D00m; PD0004048; Na/ntran_symport; 2.
PROSITE; PS00923; ASP_GLU_RACEMASE_1; UNKNOWN_1.
PROSITE; PS009610; NA_NEUROTRAN_SYMP_1; UNKNOWN_1.
PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; 1.
PROSITE; PS00754; NA_NEUROTRAN_SYMP_3; 1.
PROSITE; PS00754; NA_NEUROTRAN_SYMP_3; 1.
PROSITE; PS00754; NA_NEUROTRAN_SYMP_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine transporter type GLYT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu Q.-R., Li Q.-F.; "Cloning and expression of mouse glycine transporter 2 submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF411042; AAL17054.1; "...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                           EVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMD 422
                                                                                                                                                                                                                                                                                                                                                                    VFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNS
                                                                                                                                                                                                                                                                                                                                                                                                                         GIKSSGKVVYFTATFPYVVLVILLIRGVTLPGAGAGIWYFITPKWEKLTDATVWKDAATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                               GVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSAVTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A-ASVNNITNGT--SSAQLYFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGVVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMLALAGLPIFFLEVSLGQFASQGPVSVWKAIPALQGCGIAMLIISVLIAIYYNVIICYT
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                                                               SYVYGLORFCEDIEMMIGFKPNIFWKVCWAFVTPTILTFILCFSFYQWEPMTYG-SYRYP
                                                                                                    FWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNULVFGDNYVYP 539
                                                                                                                                                                                                                                                  IFFSLSAAWGGLITLSSYNKFHNNCYRDTLIVTCTNSATSIFAGFVIFSVIGFMANERKV 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFYLFASFYSVLPWGSCNNPWNTPECKDKTKLLLDSCVIGDHPKIQIKNSTFCMTAYPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVLLLYGKPYYYLECYLGQFSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLC
NWSMVLGWLMLACSVIWIPIMFVIKMY-LAPGRFIERLKLVCSPQPDWGPFLAQHRGE
                                       TAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPSWGPRSPRERRE
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Pred. No. 1.4e
05; Mismatches
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Last sequence update)
Last annotation update)
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Sciurognathi; Muridae;
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L.4e-78;
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; Murinae; Mus
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Indels Length

Gaps

638; 50;

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JMAS

) Q9JMA9

C9JMA9

T 01-CCT-2000 (TrEMBLrel. 15, Created)

T 01-UT-2000 (TrEMBLrel. 15, Last sequence updat

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation up?

Ecolonic system B0+ amino acid transporter.

GN SLC6A14 OR MCATBO+.

OS Mus musculus (Mouse).

CE Eukaryota; Metazoa; Chordata; Craniata; Verter

Mammalia; Eutheria; Rodentia; Sciurognathi; M
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Best Local
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01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8SYT9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY071318; AAL48940.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                 FTSFLSGCTIFGILGNLAYELNSEVGDVVGAGGTSLAFISYPDATAK-TFQPQLFSVLFF
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Last sequence up
Last annotation
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Pred. No. 3.7e-77;
3; Mismatches 97;
                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
REMBL; AB033285; BAA94300.1; -
R MGD; MGI:1890216; Slc6al4.
InterPro; IPR000175; Na/ntran_symport.
R Pfam; RP00209; SNEY 1.
R Pfam; RP00209; SNEY 1.
R PFCDOM; PD000448; Na/ntran_symport; 2.
R PROSITE; PS00610; Na_NEUROTRAN_SYMP_1; 1.
R PROSITE; PS00610; Na_NEUROTRAN_SYMP_1; 1.
R PROSITE; PS0067; Na_NEUROTRAN_SYMP_3; 1.
SEQUENCE 638 AA; 71455 MW; 5D5A78E2DF7E7612 CRC64;
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Best Local :
                                                                                           Q8WPM9 PRELIMINARY;
Q8WPM9;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-JUN-2002 (TREMBLREL 2
Similar to glycine transp
                                   BAC001.6.
Oikopleura (
Eukaryota; !
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                                                                                                                                                                                                                                                                             MIIFCIIWIPI----MAIIKIVQAEGNILQRIISCCRPASNWGPYLEKHRGERYRDMAE
                                                                                                                                                                                                                                                                                                                    MLFLGMTFVPIGIGFSLYK--YRTGTFSETIKKAFHSKPSWGPRSPRERREWMQFKAE 604
                                                                                                                                                                                                                                                                                                                                                    IEFMLGKKTGAY---WRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVSGYL
                                                                                                                                                                                                                                                                                                                                                                                                                            ITLGCCLTLFLLGLLCVTQAGIYWVHLIDHFCAGWGILIAAILEIAGIIWIYGGNRFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGVFWIYGLENLCLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAYPEALAQLPAGPFWSILFFFMLLTLGLDSQFASIETITTFQDLFPKAMKRMRVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMDAFP-----RVPTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSYNKFNNNCYSDAIIVCLTNCLTSVFAGFAIFSILGHMAHISGKEVSQVV-KSGFDLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWANCS-SWADENCSRTPIVTGCNVSIGAGEMFMNISWVNTNNLTCLNGSEVFRPGQLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LECSLGQFASLGPVSVWRILPLFQGVGITMVLISVFVAIYYNVIIAYSLYYLFASFQSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENQERGNWSKKSDYLLSMVGYAVGLGNVWRFPYLTYTNGGGAFLIPYAIMLALAGLPLFF
                                       Metazoa;
                                                                                                                                                                                     PRELIMINARY;
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                                                                                       Lrel. 20, Created)
Lrel. 20, Last sequence up
Lrel. 21, Last annotation
transporter.
                                     Chordata;
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Pred. No. 6e-7.
93; Mismatches
                                     Urochordata;
                                                                                                                                                                                     674
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6e-74;
5as 225;
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619

548 505 491 445 431 329 317

388 377 259

210

269

199

151 166 91 106 14;

update)

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Appendicularia;

Mus.

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Best Local S
Matches 226
                     Q9D317; PRELIMINARY;
Q9D317;
01-JUN-2001 (TrEMBLrel. 17
01-JUN-2001 (TrEMBLrel. 17
01-JUN-2002 (TrEMBLrel. 21
9030613J17Rik protein.
SLC6A14 OR 9030613J17RIK.
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Prodom; PD000448; NA_Ntran_symport; 1.

PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; UNKNOWN_1.

PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.

SEQUENCE 674 AA; 75155 MW; 9D318B68D64416E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF374376; AAL56437.1; -.
InterPro; IPRO00175; Na/ntran_symport.
Pfam; PF00209; SNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oikopleuridae; Oikopleura
NCBI_TaxID=34765;
Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 0:0-0(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CVLGQFSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQA----
                                                                                                                                             LYKYRTGTFSETIKKAFHSKPSWGPRSPRER
                                                                                                                                                                         LCWGVITPAIMTTVEFEYALLASNNLVFGDNYVYPT-AGYVSGYLMLFLGMTFVPIGIGFS
                                                                                                                                                                                                                     VYCTPGGQYILELVDHYGGTFLVLFCAISELAGVFWIYGLENLCLDIEFMLGKKTGAYWR
                                                                                                                                                                                                                                         TGSIVWSVLFFTMLLMLGLSTMFATMNTIITCCSDAFPQLRKRQASFTAVLCVFLFLLGI
                                                                                                                                                                                                                                                           QPQL-FSVLFFLMMSVLGIGSSVALLSTFNTLAMDAFP--RVPTVYMSAMTCSCGFLLGL
                                                                                                                                                                                                                                                                             RDTLIVVLTNSATSIFAGLTIFSYLGEMAHSMGVEVED-VARQGPGLAFIAYPEALTQIS
                                                                                                                                                                                                                                                                                       RDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNSEVGDVVGAGGTSLAFISYPDAIAKTF
                                                                                                                                                                                                                                                                                                                 GLTKDGSLNGIKYELTPEWERLKDMSVWKDAATQIFFSLSASWGGLITLASYNEFDNNIV
                                                                                                                                                                                                                                                                                                                                                      EMSDSIE-DVGLPKADLVLYLAISYAILFICLAKGIQSTGKAVYITSTFPYVVLTTLLIV
                                                                                                                                                                                                                                                                                                                                                                                          ELPWANCONSWNDEKCMDVGRLNRCRSIQANGTLEVPAMCQLNHTNREAPSQQYFENHIL
                                                                                                                                                                                                                                                                                                                                                                                                           ICWKFVSPVLLTAVFI-AVLANWKVSTLGNYVYPNWTNYPAVGLILF-SVLFIPLMAIHH
                                                                                                                                                                                                   PMTTRAGLYILTLEDDEGGSYALLVISVAEMVSICFIYGLDNECSDIQIMIKRPVGMEWR
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21,
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                                       Created)
Last sequence
Last annotation
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Pred. No. 6.4e
02; Mismatches
    Craniata;
                                         annotation
                                                  sequence update)
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6.4e-74;
    Vertebrata;
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R., C
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re genome.";
    Euteleostomi;
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; NCBI_TaxID-10090;
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nes 230; Conserv
                       446
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llarity 38.5%;
Conservative 93
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Pred. No. 1e-7
93; Mismatches
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Rawai J. Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batahov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batahov S., Casavant T.,
A Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehi R., Catulli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Havashiraki Y., Storch K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Havashiraki Y., Storch K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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"Functional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).

EMBL; AK018553; BAB31272.1; -

MGD; MGI:1890216; S1c6a14.

InterPro; IPR000175; Na/ntran_symport.

Pfam; PF00209; SNF; 1.

PRINTS; PR00176; NANEUSMPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000448; Na/ntran_symport; 2.
PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
PROSITE; NS00267; NA_NEUROTRAN_SYMP_3; 1.
SEQUENCE 638 AA; 71412 MW; 5D461554187E7612 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                           SSYNGFRHNIYRDAWIYTTLDTFTSFLSGCTIFGILGNLAYELNSEVGDVVGAGGTSLAF
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                                                                                                                                                                                                                SSYNKFNNNCYSDAIIVCLTNCLTSVFAGFAIFSILGHMAHISGKEVSQVV-KSGFDLAF
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                                                                                                                                    MSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGVFWIYGLENLCLD
                                                                                                                                                                                                                                                          ITLGCCLILFLLGLLCVTQAGIYWVHLIDHFCAGWGILIAAILEIAGIIWIYGGNRFIED
WRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVSGYL
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Searc Job t	ДУ	Db
Search completed: July 21, 2003, 09:27:47 Job time : 91 secs	549 MLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPSWGPRSPRERREWMQFKAE 604	: : ::: :: : :

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Minimum DB
Maximum DB
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: BLOOM, Allen
REGISTRATION UNMER: 29,135
REFERENCE/DOCKET NUMBER: 3177
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 609-520-3214
TELEPAX: 609-520-3259
                                                                                                                                                                                                                            APPLICATION NUMBER: USE FILING DATE: CLASSIFICATION: 536
PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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STREET: 997 Lenox Drive, Building
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
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APPLICANT: CHAPMAN, CONRAD GERALD
APPLICANT: GLOGER, ISRAEL SIMON
APPLICANT: EVANS, JOANNE RACHEL
APPLICANT: CAIRNS, WILLIAM
APPLICANT: HERDON, HUGH
TITLE OF INVENTION: NOVEL COMPOUND
FILE REFERENCE: GP-30176
CURRENT APPLICATION NUMBER: US/09/112,728A
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 981889).
PRIOR APPLICATION NUMBER: 981889).
PRIOR FILING DATE: 1998-08-28
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SOFTWARE: FastSEQ for
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; SEQ ID NO 2; LENGTH: 797; TYPE: PRT; ORGANISM: HOMO 5
                                                                                                                                                                                         APPLICANT: William Cairns
APPLICANT: William Cairns
APPLICANT: Hugh Jonathan Herdon
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: Egs-30176-D1
CURRENT APPLICATION NUMBER: US/09/795,232
CURRENT FILING DATE: 2001-02-28
CURRENT FILING DATE: 09/182,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-09-795-232-2
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                                                                                               PRIOR APPLICATION NUMBER: 09/18
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 98188
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows V
                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                              Conrad Gerald Chapman
Israel Simon Gloger
Joanne Rachel Evans
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                                                                                                                                                                                                                                                                                                                                                                                                           Anthony M. Brown
                     SAPIENS
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                                                                                                 Version
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밁 Ş Matches Query Match Best Local : Local Similarity 54 WSNNIEFLMSCIATSVGLGNVWREPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQ WSSKLDFILSMVGYAVGLGNVWRFPYLAFQNGGGAFLIPYLMMLALAGLPIFFLEVSLGQ Conservative 32.3%; 105; Score 1082.5; DB 4; Pred. No. 1.3e-93; 5; Mismatches 213; Indels Length 39; Gaps 253

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Wir
                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Borden, Laurence A.
APPLICANT: McKelvy, Jeffrey F.
TITLE OF INVENTION: Human Glycine
NAME: Bloom, Allen
RECISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                  CITY:
STATE:
                                                                                                  FILING DATE:
                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                  COUNTRY:
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997 Lenox Drive, Building
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             CURRENT APPLICATION NUMBER: US/09/191,468A
CURRENT FILING DATE: 1998-11-12
NUMBER OF SEO ID NOS: 124
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 122
LENCTH: 797
TYPE: PRT
ORGANISM: Human
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US-08-700-013B-19
                                                                                                                                                                           RESULT 5
US-09-191-468-122
                                                                                                                     Patent No. 6416975
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                                                                                                              GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: Gailagher, Michael J.
APPLICANT: Burgess, Loyd R.
APPLICANT: Brunden, Kurt R.
TITLE OF INVENTION: Human Glycine Transporter
FILE REFERENCE: 12311US01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 797 amino acid
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Pred. No. 2e-93;
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RESULT 6
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                                                  Best Loc
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                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Sequence 124, Application US/0919169A
Patent No. 6416975
                                                                            Query Match
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Best Local Similarity
Matches 220; Conserv
                                                                                                                                                                                               APPLICANT: Burgess, Loyd R.
APPLICANT: Brunden, Kurt R.
TITLE OF INVENTION: Human Glycine Transport
FILE REFERENCE: 12311US01
CURRENT FILING NUMBER: US/09/11/1,468A
CURRENT FILING DATE: 1998-11-12
CURRENT FILING DATE: 1998-11-12
CURRENT FILING DATE: 1998-11-12
CURRENT FILING DATE: 1998-11-12
                                                                                                                                                                                                                                                                                                        APPLICANT: Gallagher, Michael J.
                                                                                                                                          LENGTH: 79
TYPE: PRT
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Best Local Similarity
Matches 219; Conserv
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US-09-191-468-120
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CURRENT FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 120
LENGTH: 797
                                                                                                                                                                                                                                                                                                                                                            Sequence 120, Application US/09191468A
Patent NO. 6416975
GEMERRAL INFORMATION:
APPLICANT: Gallagher, Michael J.
APPLICANT: Burgess, Loyd R.
APPLICANT: Brunden, Kurt R.
APPLICANT: Brunden, Kurt R.
TITLE OF INVENTION: Human Glycine Transporter Type
FILE REFERENCE: 12311US01
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                                           LEVSLGQFASQGPVSVWKAIPALQGCGIAMLIISVLIAIYYNVIICYTLFYLFASFVSVL
                                                                        LECVLGQFSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATL 166
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                                                                                                                                                                   Conservative
                                                                                                                                                                               32.1%;
                                                                                                                                                                 108;
                                                                                                                                                                Score 1076.5; DB 4;
Pred. No. 4.8e-93;
)8; Mismatches 220;
               ENCVPSD
                                                                                                                                                                 Indels
                                                                                                                                                                                             Length
---PTLA-ASVNNITNGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                             NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kowalski, Leslie R.Z. APPLICANT: Borden, Laurence A. APPLICANT: MCKELY, Jeffrey F. TITLE OF INVENTION: Human Glycine NUMBER OF SEQUENCES: 41
                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
             SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acid
                                                                                     REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                         STREET: 99/ Lawrenceville
                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                          TELEFAX:
                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWGSCNNPWNTPECKDKTKLLLDSCVISDHPKIQIKNSTFCMTAYPNVTMVNFTSLANKT
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997 Lenox Drive, Building
               799 amino acids
                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                            609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Albert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vivian R.
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                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                 Sequence 8, Application US/07879617A Patent No. 5580775
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,617A
                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affinity L-Proline Transporter
NUMBER OF SEQUENCES: 13
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                                                                                                                                     STATE:
                                                                                                                                                   CITY:
                                                                          MEDIUM TYPE:
                                                                                                                      COUNTRY:
                                                                                                                                                                   STREET:
                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                   Atlanta
                                                                                                                    Georgia
Y: U.S.
                                                                                                                                                                   1100 Peachtree Street,
                                                                                                                                                                                                                                                     Fremeau Jr.,
Caron, Marc
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Suite 2800

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303 VFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNS 362
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714 NWSMVLGWLMLACSVIWIPIMFVIKMY-LAPGRFIERLKLVCSPQPDWGPFLAQHRGE 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TMVNFTSQANKTFVSGSEEYFKYFVLKISAGIEYP-GEIRWPLPFCLFLAWVIVYASLAK
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                                                       TAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPSWGPRSPRERRE 597
                                                                                                                                                                    FWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDNYVYP 539
                                                                                                                                                                                                                                                                          AFPRVPTVYMSAMT---CSCGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGV 479
                                                                                                                                                                                                                                                                                                                                                           NIENVADQ-GPGIAFVVYPEALTRLPLSPFWAIIFFLMLLTLGLDTMFATIETIVTSISD 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSAVTQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T--NGTSSA-----QLYFLRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGVVAR 242
                                                                                                                  SYVYGLQRFCEDIEMMIGFQPNIFWKVCWAFVTPTILTFILCFSFYQWEPMTYG-SYRYP
                                                                                                                                                                                                                                  EFPKYLRTHKPVFTLGCCICFFIMGFPMITQGGIYMFQLVDTYAASYALVIIAIFELVGI 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFFSLSAAWGGLITLSSYNKFHNNCYRDTLIVTCTNSATSIFAGFVIFSVIGFMANERKV 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 107;
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TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 667 amino acid
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TYPE: AMINO ACID
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMUL
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TISSUE TYPE: Brain
IMMEDIATE SOURCE:
LIBRARY: rat fore
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                                                               NAME/KEY: Domain LOCATION: 530..549 OTHER INFORMATION:
                                                                                                                           NAME/KEY: Domain
LOCATION: 487..509
OTHER INFORMATION:
                                                                                                                                                                                       NAME/KEY: Domain LOCATION: 454..473 OTHER INFORMATION:
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LOCATION:
 NAME/KEY: Domain
LOCATION: 567..589
OTHER INFORMATION:
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LOCATION: 404..427
OTHER INFORMATION:
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LOCATION: 103..127
OTHER INFORMATION:
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272..294
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147..167
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Qy	Оу	Qу	Оy	Оy	Db Qy	Db Oy	Db Qy	Db Qy	Оу	Query Best 1 Matche	US-07
536 YYYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRTGTFSETIKKAFHSKPSWGPRSPRER 595	476 LAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGDN 535	419 LAMDAFPRVPTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISE 475	359 ELNSEVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNT 418	299 AVTQVFFSLTVCTGPITNESSYNGFRHNIYRDAWIVTTLDTETSFLSGCTIFGILGNLAY 358 : : :: :	239 VVARGVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYS 298 ::	181 SDPTLAASVNNITNGTSSAQLYFLRTYLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFG 238	127 PAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEWENCVP 180	67 TSVGLGNVWREPFIAYONGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVKVWSIS 126 : :: :: :	11 ESSEPKMEPKRSSQISL-PPANNKAALDNIDDTDLEAE-PPERNYWSNNIEFLMSCIA 66	Query Match 30.7%; Score 1030.5; DB 1; Length 667; Best Local Similarity 38.7%; Pred. No. 8.3e-89; Matches 234; Conservative 94; Mismatches 255; Indels 21; Gaps 13	ATURE: NAME/KEY: Region COCATION: 44.45 OTHER INFORMATION: OTHER INFORMATION: ATURE: NAME/KEY: Region LOCATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: ATURE: NAME/KEY: Region LOCATION: 630.631 OTHER INFORMATION: ATURE:

YRFPAWAELLGILMGLLSCLMIPAGMLVAVLR-EEGSLWERLQQASRPAIDWGP-SLEEN 616

247..266

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US-08-753-985-8
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                 ANTI-SENSE: NO FRAGMENT TYPE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/879617 FILING DATE: 01-MAY-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 667 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 404-815-6508
                                                                                                                                                                                             TISSUE TYPE: Brain
IMMEDIATE SOURCE:
LIBRARY: rat forebrain cDNA library
CLONE: rTB2-2-20
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                         YPOTHETICAL:
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                                                                                LOCATION: 103..12 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                          LOCATION: 147..16 OTHER INFORMATION:
                                                     NAME/KEY:
                                                                                                            NAME/KEY:
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NAME/KEY:
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Y: U.S.
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/PE: N-terminal
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                                         Domain
147..167
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                                                                                                                                                                                                                                                                                                                                   .55: single
linear
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Domain
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                                                                                                                                       /note=
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                          "Membrane-spanning domain"
                                                                               "Membrane-spanning domain"
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                                                   Query Match
Best Local S
Matches 234
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LOCATION: 630..631
OTHER INFORMATION: OTHER INFORMATION: 1
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LOCATION: 269..270
OTHER INFORMATION: OTHER INFORMATION: I
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LOCATION:
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LOCATION:
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LOCATION:
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LOCATION:
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 23 ESEQENCEMKKLQEAHLRKPVTPDLLMTPSDQGDVDLDVDFAADRGNWTGKLDFLLSCIG
                        11 ESSEPKMEPKRSSQISL-PPANNKAALDNID--DTDLEAE-PPERMVWSNNIEFLMSCIA
                                                   Similarity 38. 34; Conservative
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272..294
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353..375
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567..589
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487..509
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530..549
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454..473
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212..213
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106..127
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                                                   30.7%; Score 1030.5; DB 1; 38.7%; Pred. No. 8.3e-89; Live 94; Mismatches 255;
                                                                                                                      /note= "N-linked glycosylation
site"
                                                                                                                                                                                                                                                                                                                 /note= "protein kinase
phosphorylation site"
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phosphorylation site"
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phosphorylation site"
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kinase phosphorylation site"
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                                                                                                                                                                                         "Leucine zipper motif"
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                                                     Indels
                                                                               Length
                                                                               667;
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                                                     Gaps
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13;

9 #	ECS & Priss	RESULT 11 US-07-879-617A-9 ; Sequence 9, Application US/0787961 A ; Sequence 9, Application US/0787961 A ; Patent No. 5580775 ; GENERAL INFORMATION: ; APPLICANT: Fremeau Jr., Robert T ; APPLICANT: Caron, Marc G. ; APPLICANT: Caron, Marc G. ; APPLICANT: Blakely, Randy D. ; TITLE OF INVENTION: A High Affin ty L-Proline Transporter NUMBER OF SEQUENCES: 13	Db 559 YRFPAWAELLGILMGLLSCLMIPASMLVAVLR-EEGSLWERLOQASRPAIDWGP-SLEEN 616 Qy 596 REWM 599	476 LAGVEWIYGLENLGLDIEFMLGKK 476 LAGVEWIYGLENLGLDIEFMLGKK 1 : :	299 AVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAY	RTVLQQSDGIEGGIGAPIWYLVLCLFIAWLMVFG	Qy 67 TSVGLGNVWREPETAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQESSRNSVKVWSIS 126
OTHER INFORMATION: /note= "Proposed transmembrane OTHER INFORMATION: domain." FEATURE: NAME/KEY: Domain LOCATION: 500519 OTHER INFORMATION: /note= "Proposed transmembrane OTHER INFORMATION: domain." FEATURE: NAME/KEY: Domain LOCATION: 536559 OTHER INFORMATION: /note= "Proposed transmembrane INFORMATION: 536559"		ATION: ER INFOR ER INFOR RE: E/KEY: ATION: ATION: ER INFOR ER INFOR	URE: WE/KEY: Domain CATION: 243264 ER INFORMATION: /note- HER INFORMATION: domain. URE: WE/KEY: Domain	FEATURE: NAME/KEY: Domain LOCATION: 117137 OTHER INFORMATION: /note= "Proposed transmembrane OTHER INFORMATION: domain." FEATURE: NAME/KEY: Domain LOCATION: 217236 OTHER INFORMATION: /note= "Proposed transmembrane OTHER INFORMATION: domain."		THETICAL: SENSE: SENSE MENT TYPE INAL SOUR JANISM: SUE TYPE JRE:	TELEFAX: 404-815-6555 ; INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 635 amino acids TYPE: AMINO ACID STRANDEDNESS: single TOPOLOGY: linear

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RESULT 12
US-08-753-985-9
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Sequence 9, Application US/08753985
Patent No. 5759788
Patent No. 5759788
GENERAL INFORMATION:
APPLICANT: Fremeau Jr., Robert T.
APPLICANT: Caron, Marc G.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affinity L-Proline Transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 QGI-GRPGEIRWNLCLCLLLAWVIVFLCILKGVKSSGRVVYFTATFPYLILLMLLVRGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 DGIEGGLGAPIWYLVLCLFIAWLMVFGVVARGVKSSGKAAYFLALFPYVVMITLFITTII 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 MSFQATLPWAICQPEW--ENCV----PSDPTLAASVNNITNGTSSAQLYFLRTVL--QQS 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 VGKPVYYLECVLGQFSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPGAMKGIQFYLTPQFHHLLSSKVWIEAALQIFYSLGVGFGGLLTFASYNTFHQNIYRDT
                                                                                                                                                                                             EEGSLWERLQQASRPAIDWGP-SLEENRTGM 590
                                                                                                                                                                                                                          RTGTFSETIKKAFHSKPSWGPRSPRERREWM 599
                                                                                                                                                                                                                                                                                        GVITPAIMTTVFFYALLASNNLVFGDNYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKY
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Pred. No. 1.5e-87;
11; Mismatches 237;
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                     NAME/KEY:
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LOCATION: 217..236
OTHER INFORMATION: /
OTHER INFORMATION: d
FEATURE:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acid
OTHER INFORMATION: OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
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APPLICATION NUMBER: U
FILING DATE: 01-MAY-
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                                                                                 NAME/KEY: Domain LOCATION: 243..264 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                          NAME/KEY: Domain LOCATION: 117..137 OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
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FILING DATE: 03-DEC-1996
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STATE: Georgia
                                         LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
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TRY: U.S.
30309
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1100 Peachtree Street, Suite 2800
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01-MAY-1992
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Domain 322..345

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Query Match
Best Local :
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LOCATION: 536..559
OTHER INFORMATION: OTHER INFORMATION:
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LOCATION: 500..519
OTHER INFORMATION: OTHER INFORMATION:
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LOCATION: 456..479
OTHER INFORMATION: OTHER INFORMATION:
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LOCATION:
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    324
                                                        264
                                                                                  272
                                                                                                             205
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                                                                                                                                                                                                                                            100 VGKPVYYLECVLGQFSSRNSVK∭W∯ISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLA 159
                                                                                                                                                                                                                                                                             26
                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEY: Active-site ION: 83.84 /nc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                  WIVTTLDTFTSELSGCTIEGILGNIAYELNSEVGDVVGAGGTSLAFISYPDAIAKTEQPQ 391
 FIVTLGNAITSILAGFAIFSVLdvijSQELGVPV-DQVAKAGPGLAFVIYPQAMTMLPLSP 382
                                                     LPGAWKGIQFYLTPQFHHLLSS#V#IEAALQIFYSLGVGFGGLLTFASYNTFHQNIYRDT
                                                                              LPGATDGILFFVTPQWAKLLELQVYYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDA 331
                                                                                                          QGI-GRPGEIRWNLCLCLLLAW||T||FLCILKGVKSSGRVVYFTATFPYLILLMLLVRGVT
                                                                                                                                     DGIEGGLGAPIWYLVLCLFIAWIM FGVVARGVKSSGKAAYFLALFPYVVMITLFITTII 271
                                                                                                                                                                ASLYSNLPWEHCGNWWNTERCLEH GPKDGNGALPL-NLSSTVSPSEEYWSRYVLHIQGS 204
                                                                                                                                                                                           MSFQATLPWAICQPEW -- ENCV --
                                                                                                                                                                                                                   CGIPLEFLELSLGOFSSLGPLA WHISPLEKGAGAAMLLIVGLVAIYYNMIIAYVLFYLF 145
                                                                                                                                                                                                                                                                          DVDLDVDFAADRGNWTGKLDFL#S#IGYCVGLGNVWRFPYRAYTNGGGAFLVPYFLMLAI 85
                                                                                                                                                                                                                                                                                          DTDLEAE-PPERMVWSNNIEFLHSKIATSVGLGNVWRFPFIAYQNGGGAFLVPYVIVLLL 99
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373..397
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No. 1.5e-87;
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RESULT 13
US-08-301-722A-5
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                      Query Match
Best Local
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APPLICANT: Uhl, G
                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPUTER: COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
CURRENT APPLICATION UNMBER: US/08/301,722A
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               HYPOTHETICAL:
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                                                                                                                                                                  FEATURE:
                                                                                                                                                                               FRAGMENT TYPE:
                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
 Local Similarity nes 213; Conserv
                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: not
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                                                                                                                           LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
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                                                                                                                                              NAME/KEY:
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 Pred. No. 4.9e.
8; Mismatches
Score 1011; DB 1;
Pred. No. 4.9e-87;
8; Mismatches 229;
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RESULT 14
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APPLICANT: Smith,
APPLICANT: Borden,
APPLICANT: Hartig,
APPLICANT: Weinsha
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1:
Patent No.
                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DNA ENCODING
TITLE OF INVENTION: DNA ENCODING
TITLE OF INVENTION: TRANSPORTERS
NUMBER OF SEQUENCES: 35
                                                                                SOFTWARE: PatentIn Release #1.30 CURRENT APPLICATION DATA:
                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                              STATE: N
                                                                                                                                                                                                                              STREET:
                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   APPLICATION NUMBER: FILING DATE: DECEME CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYVYPTAGYVSGYLMLFLGMTFVPIGIGFSLYKYRT--GTFSETIKKAFHS-----KPSW 587
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                                                                                                                                                                                                                                                                                                                                       Borden, Laurence A.
Hartig, Paul R.
Weinshank, Richard
                                                                                                                                                                                                USA
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                                                                                           Sequence 4, Application Patent No. 5756348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
 APPLICANT:
                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212-2, TELEPHONE: 212-391-0525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 DGQI-----STEVSEAPVASDKPKTLVVKVQKKAGDLPDRDTWKGRFDFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEW--ENCV 179
                                                                                                                                                                                                                         GPRSPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARGVKSSGKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSA
                                                                                                                                                                                                                                                       SYVFPKWGQGVGWLMALSSMVLIP----GYMAYMFLTLKGSLKQRLQVMIQPSEDIVRPEN
                                                                                                                                                                                                                                                                                                                     ECVSISWEYGVNREYDNIQEMVGSRPCIWMKLCWSFFTPIIVAGVFLFSAVQMTPLTMG-
                                                                                                                                                                                                                                                                                                                                                                                                                 AMDAFPRV----PTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFL-VLFCAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                TKRSIAD-VAASGPGLAFLAYPEAVTQLPISPLWAILFFSMLLMLGIDSQFCTVEGFITA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNSEVGDVVGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATQIFFSYGLGLGSLIALGSYNSFHNNVYRDSIIVCCINSCTSMFAGFVIFSIVGFMAHV
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                                                                                                                                                                                                                                                                                                                                                 ELAGVFWIYGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTTVFFYALLASNNLVFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VWKLAPMFKGVGLAAAVLSFWLNIYYIVIISWAIYYLYNSFTTTLPWKQCDNPWNTDRCF
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 Weinshank,
               Hartig,
                              Branchek,
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                                                               Smith,
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Richard
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Pred. No. 9.5e-87;
2; Mismatches 231;
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582

587 525 534 466 474

348

359 288 299 228

Db 408 LVDEYPRLLRNRRELFIAAV-C: VYLIGLSNITQGGIYVFKLFDYYSASGMSLLFLVFF 466	- CSC	Qy 360 LNSEVGDVVGAGGTSLAFISYDDAJAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTL 419 :	Qy 300 VTQVEFSLTVCTGPIIMFSSYNGERHNIYRDAWIVTTLDTETSFLSGCTIFGILGNLAYE 359	Qy 240 VARGVKSSGKAAYFLALFPYVVNITILFITTIILPGATDGILFFVTPQWAKLLELGVWYSA 299	QY 180 PSDPTLAASVNNITNGTSSAQLYFIRTVLQQSDGIEGGLGAPIWYLVLCLFIAWLMVFGV. 239	Qy 122 VWSISPAMKGTGYAQAAGCGYI SIYVVICGLCLYYLAMSFQATLPWAICQPEWENCV 179 :	Oy 62 MSCIATSVGLGNVWREPFIAYONG(GAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVK 121 : : :: : ::	Qy 3 DGQVNGGFESSEPKMEPKRSSQ\S\:\LPPANNKAALDNIDDTDLEAEPDERMVWSNNIEFL 61	Query Match 30.1%; Score 1008; DB 1; Length 599; Best Local Similarity 34.8%; Pred No. 9.5e-87; Matches 211; Conservative 122; Mismatches 231; Indels 42; Gaps 13;	TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: N FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: RAT GABA TRANSPORTER US-08-240-783B-4 (GAT-1)	ON INFORMATION: 212) 278-0400 2)391-0525 EQ ID NO: 4: TERISTICS: amino acids acid	800 ORMATION: hn P. 28,678 BER: 28,678	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-TOS SOFTWARE: Patentin Release #	ADDRESSEE: Cooper & Dunham LIP STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036	TITLE OF INVENTION: THEREOF : NUMBER OF SEQUENCES: 8	
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Search completed: July 21, 2003, 09:28:09 Job time: 20 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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3354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNDGQVNGGFESSEPKMEPK.....TSRVKHLWYSITGAYRRNIN 633
                                                                                                                      10:
11:
12:
13:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match I	Length I	DB	ID	Description
	1082.5	32.3	797	10	US-09-795-232-2	Sequence 2, Appli
N	1025.5	30.6	624	10	us-09-795-693-24	Sequence 24, Appl
ω	1025.5	30.6	624	15	US-10-156-239-24	Sequence 24, Appl
4	1025.5	30.6	624	15	US-10-199-485-24	Sequence 24, Appl
5	991	29.5	630	10	US-09-843-598-10	Sequence 10, Appl
0	971	29.0	622	10	US-09-843-598-11	Sequence 11, Appl
7	953.5	28.4	587	11	US-09-815-923-4	Sequence 4, Appli
8	932.5	27.8	614	12	US-09-919-039-378	Sequence 378, App
9	929.5	27.7	597	11	US-09-815-923-14	Sequence 14, Appl
10	882	26.3	727	11	US-09-815-923-10	Sequence 10, Appl
11	869	25.9	556	11	US-09-815-923-6	Sequence 6, Appli
12	852.5	25.4	671	10	US-09-843-598-5	Sequence 5, Appli
13	844.5	25.2	671	10	US-09-843-598-7	Sequence 7, Appli
14	833	24.8	676	11	US-09-815-923-12	Sequence 12, Appl
15	790	23.6	730	10	US-09-741-149-2	Sequence 2, Appli
16	790	23.6	730	10	US-09-795-693-5	Sequence 5, Appli

	23.6 730 15 US-10-199 23.5 730 10 US-09-861 23.2 599 11 US-09-862 22.9 727 10 US-09-822 22.9 437 11 US-09-862 22.5 437 15 US-10-218 22.5 437 15 US-10-218 22.5 459 11 US-09-818 22.5 459 11 US-09-818 22.5 459 12 US-09-84 11.7 421 10 US-09-84 12.7 421 10 US-09-84 13.8 196 12 US-09-76 14.0 529 11 US-09-86 15 US-10-118 18.1 196 12 US-09-86 196 12 US-09-86 197 10 US-09-86 198 199 11 US-09-81 198 199 11 US-09-81 199 10 US-09-81 199 11 US-09-81 199 11 US-09-81 199 11 US-09-81	45	44	43	42	41								<u>ω</u>		31													
.6 730 15 US-10-199 .5 729 11 US-09-861 .9 727 10 US-09-862 .9 727 10 US-09-862 .5 437 11 US-09-816 .5 459 11 US-09-816 .5 459 15 US-10-216 .5 459 15 US-10-216 .5 459 15 US-10-216 .5 459 15 US-09-84 .6 449 12 US-09-73 .6 449 12 US-09-73 .6 449 12 US-09-73 .6 449 12 US-09-73 .6 449 12 US-09-86 .7 111 US-09-86 .8 196 12 US-09-86 .9 10 US-09-86 .1 111 14 US-09-86 .6 1111 14 US-09-86 .6 1111 14 US-09-86 .7 10 US-09-87 .4 400 11 US-09-81 .5 3 431 10 US-09-81 .3 431 10 US-09-81	.6 730 15 US-10-199-485-5 Sequence 5 729 11 US-09-741-149-4 Sequence 2 599 11 US-09-861-846-2 Sequence 9 610 11 US-09-861-846-2 Sequence 9 610 11 US-09-861-846-2 Sequence 5 437 15 US-10-216-441-4 Sequence 5 437 15 US-10-216-441-4 Sequence 5 437 15 US-10-216-441-2 Sequence 5 459 11 US-09-818-656A-2 Sequence 5 459 11 US-09-788-787-110 Sequence 5 459 11 US-09-789-787-110 Sequence 6 449 12 US-09-789-787-110 Sequence 7 724 10 US-09-843-598-6 Sequence 8 105-10-183-116-27 Sequence 105-10-183-116-27 Sequence 105-10-183-116-27 Sequence 1111 US-09-781-781-79-78-	110	110.5	111.5	111.5	112	112.5	112.5	113	113.5	114.5	120.5	127	128	128.5	133	274	321.5	469	594.5	755	755	755	755	767.5	768.5	177.5	787.5	790
15 US-10-19 10 US-09-741 11 US-09-861 11 US-09-862 11 US-09-861 11 US-09-812 11 US-09-812 11 US-09-812 11 US-09-814 11 US-09-814 11 US-09-76 10 US-09-84 11 US-09-78 12 US-09-78 13 US-09-81 14 US-09-81 15 US-10-18 15 US-10-18 16 US-09-81 17 US-09-81 18 US-09-81 19 US-09-81	15 US-10-199-485-5 10 US-09-741-149-4 11 US-09-861-846-2 11 US-09-861-846-2 12 US-09-861-846-2 13 US-09-861-846-2 14 US-09-861-846-2 15 US-09-861-6568-4 15 US-10-216-441-4 15 US-09-818-6568-4 15 US-10-216-441-2 16 US-09-813-598-6 17 US-09-815-242-11936 18 US-09-815-242-1890 19 US-09-815-242-1801 10 US-09-815-242-1801 11 US-09-815-242-1801 12 US-09-815-242-1801 13 US-09-815-242-1801 14 US-09-815-242-1801 15 US-09-815-242-1801 16 US-09-815-242-1801 17 US-09-815-242-1801 18 US-09-815-242-1801 19 US-09-815-242-800 25 US-09-815-242-800																		14.0	17.7	22.5	22.5	22.5	22.5	22.9	22.9	23.2	23.5	23.6
US-10-199 US-09-861 US-09-922 US-09-922 US-09-811 US-09-811 US-10-211 US-10-211 US-09-814 US-09-73 US-09-74 US-09-78 US-10-155	US-10-199-485-5 US-09-741-149-4 US-09-861-846-4 US-09-961-846-2 US-09-9161-846-2 US-09-916-656A-2 US-09-818-656A-2 US-09-818-656A-2 US-09-818-656A-2 US-10-216-441-2 US-09-818-656A-2 US-09-738-626-4648 US-09-738-626-4648 US-09-738-116-27 US-09-813-116-27 US-09-813-116-27 US-09-813-116-27 US-09-813-116-27 US-09-813-116-27 US-09-813-116-27 US-09-813-116-27 US-09-813-116-27 US-09-815-242-11824 US-09-815-242-11936	609	431	.476	471	497	400	84	658	755	619	1111	52	196	305														
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ALIGNMENTS

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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 797
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-795-232-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-09-795-232-2
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APPLICANT: Hugh Jonathan Herdon
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30176-D1
CURRENT APPLICATION NUMBER: US/09/795,232
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/182,728
PRIOR APPLICATION NUMBER: 09/182,728
PRIOR APPLICATION NUMBER: 9818890.7
PRIOR APPLICATION NUMBER: 9818890.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09795232 Patent No. US20010012627A1
                                                                                                                                                         Matches 222;
                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                            254 FASQGPVSVWKAIPALQGCGIAMLIISVLIAIYYNVIICYTLFYLFASFVSVLPWGSCNN 313
                                     114 FSSRNSVKVWSISPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anthony M. Brown
Conrad Gerald Chapman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Israel Simon Gloger
Joanne Rachel Evans
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                               1998-08-28
                                                                                                                                                         32.3%; Score 1082.5; DB 10; Length 797; 38.3%; Pred. No. 1.6e-89; tive 105; Mismatches 213; Indels 39;
                                                                                                                                                             Gaps
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Mon

447 419

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APPLICANT: Glucksmann, Maria A.

TITLE OF INVENTION: 20685, 579, 1714, 23821, 33894,

TITLE OF INVENTION: 32613, NO. U$21020068710A1e1 Hun

FILE REFERENCE: 35800/209292

CURRENT APPLICATION NUMBER: U$2/09/75,693

CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 60/185,966

PRIOR APPLICATION NUMBER: 60/185,966

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 624

TYPE: PRT

ORGANISM: Artificial Sequence
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US-09-795-693-24
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 234; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/09795633
Patent No. US20020068710A1
                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                         51
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                                                                                                                                              LGQFSSRNSVKVW-------SI SPAMKGTGYAQAAGCGYILSYYVVICGLCLYYLAMS
                                                                                                                                                                                                                 RMVWSNNIEFLMSCIATSVGLGNWRFFFTAYQNGGGAFLVPYYTVLLLVGKPVYYLECV
       LQ--QSDGIEGGLGAPIWYLVLC|LE||tamlmvegvvargvks-sgkaayelalepyvvmit
                                         FTTELPWATCNNSWNTPNCVEERFABNSTNGSLAALSSKNLTDYTLERTSPVEEFWERGV
                                                                                FQATLPWAICQPEWE -- NCV--
                                                                                                              LGQYTREGSITVWRKKILDKGKGTCFLFKGIGYASIVIAFYIGIYYNVIIAWALYYLFSS
                                                                                                                                                                                   RETWSGKLDEVLSVVGEAVGLGNVMREPYLCYKNGGGAFLIPYLIFLIVAGIPLFFLELA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EALTRLPLSPEWAIIFFLMLLT LG LDTMFATIETIVTSISDEFPKYLRTHKPVFTLGCCI
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Pred No. 1.7e-
94; Mismatches
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No. 1.7e-84;
smatches 201; I
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                                                                         -PSDPTLAA-SVNNITN----GTSSAQLYFLRTV
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                                                                                                                                                                                                                                                                                            Length 624;
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                                                                                                                                                                                                                                                         Gaps
                                         180
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                                                        ; OTHER INFORMATION: US-10-156-239-24
                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 09/795,693
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/185,906
PRIOR APPLICATION NUMBER: 60/185,906
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/809,557
PRIOR APPLICATION NUMBER: 60/192,018
PRIOR APPLICATION NUMBER: 60/192,018
PRIOR APPLICATION NUMBER: 60/192,018
PRIOR APPLICATION NUMBER: 60/192,018
PRIOR FILING DATE: 2000-03-24
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US-10-156-239-24
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Query Match
Best Local Similarity
                                                                                                                                            SEQ ID NO 24
LENGTH: 624
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                                                                                                                                                                            PRIOR FILING DATE: 20
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09 308,568
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 07 3 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kapeller-Libermann, Rosana TITLE OF INVENTION: No. US20030036074Alel Nucleic Acid Sequences Encoding Human Tr TITLE OF INVENTION: ATPASE Molecule, A Human Ubiquitin Hydrolase-Like Molecule, A TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor TITLE REFERENCE: 35800/247645
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/191;781 PRIOR FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Glucksmann, Maria A. APPLICANT: Kapeller-Libermann,
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191,790 PRIOR FILING DATE: 2000-03-24
                                                                                           FEATURE:
                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/808,767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FWAVLFFLMLLTLGLDSQFGGVEGIITALVDEFPILLRKVRRELFILLVCVISFLLGLFM 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLIRGVTLPGAADGIKFYLTPDFSKLLDPQVWIDAATQIFFSLGIGFGVLIALASYNKFH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CWKFVSPLILLFLFIFSIVQYGLKPLTYNNWIKEAEDYVYPNWANALGWLLALSSMLCVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTPGGQYILELVDHYGGT-FLVLFCAISELAGVFWIYGLENLCLDIEFMLGKKTGAYWRL 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFSVLFFLMMSVLGIGSSVALLSTFNTLAMDAFP----RVPTVYMSAMTCSCGFLLGLVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNLSALTADYSVYDVISEVAESEFVLGLACLEDELDKVQAGPGLAFIAYPEAVTMLPLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNIYRDAWIVTTLDTETSFLSGCTIFGILGNLA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKLSESSGIE-DLGELRWELTLCLLLAWIVVYFCLWKGVKSGSGKVVYFTATFPYVVLIV
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                                                                                                                                                                            for Windows Version
                                                                                                                                                                                                                                                   2001-03-15
                                                                   Pfam consensus
 30.6%;
 Score
Pred.
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                                                                   sequence
1025.5; DB
No. 1.7e-84;
                15;
              Length 624,
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Matches

234;

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APPLICANT: Silos-Santiago, Innaculada
ITILE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
ITILE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
ITILE OF INVENTION: 32613, No. US20030077626A1e1 Human Transporters
FILE REFERENCE: 35800/249468
CURRENT APPLICATION NUMBER: US/10/199,485
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 09/795,693
PRIOR APPLICATION NUMBER: 09/795,693
PRIOR APPLICATION NUMBER: 60/185,906
PRIOR APPLICATION NUMBER: 60/185,906
PRIOR APPLICATION NUMBER: 60/185,906
PRIOR FILING DATE: 2000-02-29
INUMBER OF SEO ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
TYPE: DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-199-485-24
; Sequence 24, Application US/10199485
; Publication No. US20030077626A1
; GENERAL INFORMATION:
                                 TYPE: PRT
ORCANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Pfam consensus
:-10-199-485-24
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Glucksmann, Maria A. APPLICANT: Silos-Santiago, Inm
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                                                                                                                                                     SOFTWARE: FastSEQ
SEQ ID NO 10
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Ranganathan, Raje
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09843598 Patent No. US20020010944A1
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/843,598
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200,549
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEO ID NOS: 11
                                                                                                                                                                                                                                                                                                                       APPLICANT: Ranganathan, Rajesh
TITLE OF INVENTION: COSERT GENES,
TITLE OF INVENTION: COMPOUNDS
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                                                                                                              LENGTH: 6:
TYPE: PRT
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  Score 991; DB 10;
Pred. No. 2.3e-81;
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Pred. No. 1.7e-84;
'4; Mismatches 201; J
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Sequence 11, Application US/09843548
Patent No. US20020010944A1
GENERAL INFORMATION:
APPLICANT: HORVITZ, H. ROBERT
APPLICANT: Ranganathan, Rajesh
FITLE OF INVENTION: COMPOUNDS
FITLE OF INVENTION: COMPOUNDS
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                                                                                                                                       FILE REFERENCE: 01997/525002
CURRENT APPLICATION NUMBER: US/09/8 3,
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200 54
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
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TYPE: PRT
ORGANISM: Drosophila melanogaste:
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SEQ ID NO 4
LENGTH: 587
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                                                                                          Matches
                                                                                                                  Query Match
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APPLICANT: Ross, Linda S.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A
TITLE OF INVENTION: Target Sites for Insecticides
FILE REFERENCE: 023070-093800US
FILE REFERENCE: 023070-093800US
                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/815,923
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                            ORGANISM: Manduca FEATURE:
                                                                                                                                                                                                             TYPE: PRT
                                                                                                      Local Similarity
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                                                                                                                                                                                                       Query Match
Best Local S
Matches 208
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SOFTWARE: PERL Program
SEQ ID NO 378
LENGTH: 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 378, Application US/09919039 Publication No. US20030108871A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030108871A1 5834958CD1
:-09-919-039-378
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kaser, Matthew R. TITLE OF INVENTION: GENES EX FILE REFERENCE: PA-0035 US
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 61
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                      Local Similarity
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                        131
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 GTGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEW--ENCVP-SDFTLAA
                                                       GNVWRFPYLCYKNGGGAFFIPYFIFFFVCGIPVFFLEVALGQYTSQGSVTAWRKICPLFQ
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PYICYQNGGGAFLIPYCVMLLFGGLPLFFLELALGQYHRCGCLTLMKRICPALKGVGYAI 124
                                                                                           GNVWRFPF IAYONGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVKVW-SISPAMK
                                                                                                                             MDGKVAVQEYGPPAVSWVPEEGEKLDQEDEDQVK----DRGQWTNKMEFVLSVAGEIIGL
                                                                                                                                                                 MEPKRSSQISLPPA----NNKAALDNIDDTDLEAEPPERMYWSNNIEFLMSCIATSVGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGCGYILSYYVVICGLCLYYL---AMSFQATLPWAICQPEWEN--CVPSDPTLAASVNN 191
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                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                       116;
                                                                                                                                                                                                                      Score 932.5; DB 1
Pred. No. 4.6e-76;
                                                                                                                                                                                                     Mismatches 241;
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                                                                                                                                                                                                                                       DB 12;
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US-09-815-923-14
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SEQ ID NO 14
LENGTH: 597
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Best Local
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                                                                                                                                                                                                                      Matches
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CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ross, Linda S.

APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A
TITLE OF INVENTION: Target Sites for Insecticides
FILE REFERENCE: 023070-093800US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gill, Sarjeet S.
                                                                                                                                                                                                                                                                                                                             ORGANISM: Manduca sexta FEATURE:
                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                    132 TGYAQAAGCGYILSYYVVICGLCLYYLAMSFQATLPWAICQPEWENCVPSDP-----TL
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                                                                      56 GNVWRFPYLCYKNGGGAFLIPYFLTLFLAGIPMFFMELAMGOMLTIGGLGVFKIAPIFKG
                                                                                           72 GNVWRFPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQFSSRNSVKVWSISPAMKG 131
                                                                                                                                                                 17 MEPKRSS----QISLPPANNKAALDNIDDTDLEAEPPERMYWSNNIEFLMSCIATSVGL
                                                                                                                                              METKNDSRSDDIELSAQGSGNKPS-----DVAVKSNLPERGSWASKLDFILSVIGLAIGL 55
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IGYAAAVMSCWMNVYYIVILAWAIFYFFMSMRSDVPWRNCDNYWNTATCVNPYDRKNLTC
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                                                                                                                                                                                                                                                                                                            GABA transporter
                                                                                                                                                                                                                                     27.7%; Score 929.5; DB 1 34.0%; Pred. No. 8.4e-76;
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US-09-815-923-10
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APPLICANT: Ross, Linda S.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Use of Insect Coll Membrane Transporters as No. US20020197644A1e1
TITLE OF INVENTION: Target Sites for Insecticides
FILE REFERENCE: 023070-093800US
CURRENT APPLICATION NUMBER: US/09/8:5,923
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 727
TYPE: PAT
ORGANISM: Manduca sexta
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Best Local
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                    NGTSS-AQLYFLRTVLQQSDGIH-\GGLGAPIWYLVLCLFIAWLMVFGVVARGVKSSGKA 250
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NGSQTPTEQFFERKVLNMSAGIEXEGGMR---WELAACLVCAWVLVYFALWKSIKSSAKV
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No. 2.3e-71;
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US-09-815-923-6
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; LENGTH: 556
; TYPE: PRT
; ORGANISM: Manduca s
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Matches
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APPLICANT: Ross, Linda S.
APPLICANT: The Regents of the University of California PITLE OF INVENTION: Use of Insect Cell Membrane Transporters TITLE OF INVENTION: Target Sites for Insecticides FILE REFERENCE: 023070-093800US CURRENT APPLICATION NUMBER: US/09/815,923 CURRENT FILING DATE: 2001-03-23 NUMBER OF SEO ID NOS: 20 NUMBER OF SEO ID NOS: 20 SOFTWARE: Patentin Ver. 2.1
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                                                AKLLELGVWYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGC 347
                                                                                     CNLICWILVYLCICNGVKSVGKIVYFTVLFPYVVLSVLFVRGITLPGAWKGIMFYILPDW
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                AQLAKPKVWADAATQIFFSLGPGWGGLVSMSSFNKFHYNNLRSSMIIPIVNSATSIWAGF
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200,549
PRIOR FILING DATE: 2000-04-26
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APPLICANT: Ranganathan, Rajesh
TITLE OF INVENTION: CESERT GENES,
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: 0197/525002
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ORGANISM: Caenorhabditis elegans
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VGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMD--AFP
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                                                          GPGFGVLLALSSYNDFNNNCYRDAVTISIINCATSFFSGCVVFSTLGYMSLLTNKPINEV
                                                                                               TVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGCTIFGILGNLAYELNSEVGDV
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                                                                                                                                   GKIVWVTATAPYIILSILLIRGLLLPGAKNGLYYYVTPDFEKLKDPAVWSAAATQIFFSL
                                                                                                                                                                                                              RNGTPLTTPSEEYYLYKVLEVQKSTGFD-DLGGVKTSMAVCLLAVFIMVVFALWKGPQSS
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Pred. No. 9.7e-69;
4; Mismatches 256;
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US-09-843-598-7
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US-09-843-598-7
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APPLICANT: Horvitz, H. Robert
APPLICANT: Ranganathan, Rajesh
TITLE OF INVENTION: CESERT GENES, PROTEINS,
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/843,598
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200,549
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
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                  483
                                                                                           423
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                                                                                                                                                                                                                                                                                   248
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          SKNRKWFYLVICIIYYFLSFPAISYGGQFVIPFLDEYGVSLSVLFIVTCEMIAVCWFYGV
                                                                                                                     VGAGGTSLAFISYPDAIAKTFQPQLFSVLFFLMMSVLGIGSSVALLSTFNTLAMD--AFP
                                                                                                                                                                                    TVCTGPIIMFSSYNGFRHNIYRDAWIVTTLDTFTSFLSGČTIFGILGNLAYELNSEVGDV
                                          RVPTVYMSAMTCSCGFLLGLVYCTPGGQYILELVDHYGGTFLVLFCAISELAGVFWIYGL 485
                                                                                                                                                            GPGFGVLLALSSYNDFNNNCYRDAVTISIINCATSFFSGCVVFSTLGYMSLLTNKPINEV
                                                                                                                                                                                                                                                                       GKAAYFLALFPYVVMITLFITTIILPGATDGILFFVTPQWAKLLELGVWYSAVTQVFFSL
                                                                                 VGEHDASLIFIVYPQALATMDYSCFWSFIFFVMLITLGIDSTFAGIEAFITGFCDESRFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WREPFIAYQNGGGAFLVPYVIVLLLVGKPVYYLECVLGQESSRNSVKVW-SISPAMKGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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APPLICANT: Gill, Sarjeet S.

APPLICANT: Ross, Linda S.

APPLICANT: The Regents of the University of TITLE OF INVENTION: Use of Insect (ell Membritle OF INVENTION: Target Sites of Insect FILE REFERENCE: 023070-093800US CURRENT APPLICATION UNMBER: US/09/31,923 CURRENT FILING DATE: 2001-03-23 NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 12

LENGTH: 676
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US-09-815-923-12
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Best Local
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ORGANISM: Manduca sexta
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                                503
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                                                                                                                                                                                                                                                       DAWIVTTLDTETSELSGCTIFGTLQNLAY-----
                                                                                                                                                                                                                                                                                                              IILPGATDGILFFVTPQWAKLLHLGWYSAVTQVFFSLTVCTGPIIMFSSYNGFRHNIYR
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                                                                                             LLSLGLGSQIGIMEGMLCTIFD DEFKRLSKPVITGVVCTFCFFVGLIFTTGAGEYWLKM
                                                                                                                            MSVLGIGSSVALLSTF - - NTLAND
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 VFFYAL -- LASNNLVFGD---
                                FDSFAGTIGLVVVALLKMIAVI | I | GHEKFINDIYEMTGYRPGIYWQVTWRYVGPAIVTC
                                                               VDHYGGTFLVLFCAISELAGVFWINGLENLCLDIEFMLGKKTGAYWRLCWGVITPAIMTT
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10. US20020197644A1
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95; Wismatches 204;
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No. 5.8e-67;
                                                                                                                              FPRVPTVYMSAMTCSCGFLLGLVYCTPGGQYILEL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                         PTLAASVNNITNGT-----SSAQLYF-LRTVLQ
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    --NYVYPTAGYVSGYLMLFLGMTFVPI
                                                                                                                                                                               ---GAGGTSLAFISYPDAIAKTFQPQLFSVLFFLM
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APPLICANT: LI, Zhenya et al

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: C1000780

CURRENT APPLICATION NUMBER: US/09/741,149

CURRENT FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 730
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; ORGANISM: Human
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                                       ASVVNMGLSPPGYNAWIEDKASEEFLSYPTWGLVVCVSLVVFAILPVPV
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hes 218;
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